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 Gerritsen, Mary E.
 Goddard, Audrey
 Godowski, Paul J.
 Grimaldi, J. Christopher
 Gurney, Austin L.
 Hillan, Kenneth J
 Kljavin, Ivar J.
 Kuo, Sophia S.
 Napier, Mary A.
 Pan, James;
 Paoni, Nicholas F.
 Roy, Margaret Ann
 Shelton, David L.
 Stewart, Timothy A.
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10015477-102501

50	55	60
Phe Phe Thr Gly Pro Met Ser Asp Phe	Lys Asn Val Gly Leu Val	
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Phe Val Asn Ser Lys Arg Asp Arg Thr	Lys Ala Val Leu Cys Met	
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Val Val Ala Gly Ala Ile Ala Ala Val	Phe His Thr Leu Ile Ala	
95	100	105
Tyr Ser Asp Leu Gly Tyr Tyr Ile Ile	Asn Lys Leu His His Val	
110	115	120
Asp Glu Ser Val Gly Ser Lys Thr Arg	Arg Ala Phe Leu Tyr Leu	
125	130	135
Ala Ala Phe Pro Phe Met Asp Ala Met	Ala Trp Thr His Ala Gly	
140	145	150
Ile Leu Leu Lys His Lys Tyr Ser Phe	Leu Val Gly Cys Ala Ser	
155	160	165
Ile Ser Asp Val Ile Ala Gln Val Val	Phe Val Ala Ile Leu Leu	
170	175	180
His Ser His Leu Glu Cys Arg Glu Pro	Leu Leu Ile Pro Ile Leu	
185	190	195
Ser Leu Tyr Met Gly Ala Leu Val Arg	Cys Thr Thr Leu Cys Leu	
200	205	210
Gly Tyr Tyr Lys Asn Ile His Asp Ile	Ile Pro Asp Arg Ser Gly	
215	220	225
Pro Glu Leu Gly Gly Asp Ala Thr Ile	Arg Lys Met Leu Ser Phe	
230	235	240
Trp Trp Pro Leu Ala Leu Ile Leu Ala	Thr Gln Arg Ile Ser Arg	
245	250	255
Pro Ile Val Asn Leu Phe Val Ser Arg	Asp Leu Gly Gly Ser Ser	
260	265	270
Ala Ala Thr Glu Ala Val Ala Ile Leu	Thr Ala Thr Tyr Pro Val	
275	280	285
Gly His Met Pro Tyr Gly Trp Leu Thr	Glu Ile Arg Ala Val Tyr	
290	295	300
Pro Ala Phe Asp Lys Asn Asn Pro Ser	Asn Lys Leu Val Ser Thr	
305	310	315
Ser Asn Thr Val Thr Ala Ala His Ile	Lys Lys Phe Thr Phe Val	
320	325	330
Cys Met Ala Leu Ser Leu Thr Leu Cys	Phe Val Met Phe Trp Thr	
335	340	345

Pro Asn Val Ser Glu Lys Ile Leu Ile	Asp Ile Ile Gly Val Asp	350	355	360
Phe Ala Phe Ala Glu Leu Cys Val Val	Pro Leu Arg Ile Phe Ser	365	370	375
Phe Phe Pro Val Pro Val Thr Val Arg	Ala His Leu Thr Gly Trp	380	385	390
Leu Met Thr Leu Lys Lys Thr Phe Val	Leu Ala Pro Ser Ser Val	395	400	405
Leu Arg Ile Ile Val Leu Ile Ala Ser	Leu Val Val Leu Pro Tyr	410	415	420
Leu Gly Val His Gly Ala Thr Leu Gly	Val Gly Ser Leu Leu Ala	425	430	435
Gly Phe Val Gly Glu Ser Thr Met Val	Ala Ile Ala Ala Cys Tyr	440	445	450
Val Tyr Arg Lys Gln Lys Lys Lys Met	Glu Asn Glu Ser Ala Thr	455	460	465
Glu Gly Glu Asp Ser Ala Met Thr Asp	Met Pro Pro Thr Glu Glu	470	475	480
Val Thr Asp Ile Val Glu Met Arg Glu	Glu Asn Glu	485	490	

<210> 8
 <211> 535
 <212> DNA
 <213> Homo sapiens

<220>
 <221> unsure
 <222> 33, 66, 96, 387
 <223> unknown base

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 cggcctattg tcaacctctt tgtttcccg gaccttggtg gcagttctgc 150
 agccacagag gcagtggcga ttttgacagc cacataccct gtgggtcaca 200
 tgccatacgg ctggttgacg gaaatccgtg ctgtgtatcc tgctttcgac 250
 aagaataacc ccagcaaca actggtgagc acgagcaaca cagtcacggc 300
 ggccacatc aagaagttca ccttcgtctg catggctctg tcaactcacgc 350
 tctgtttcgt gatgttttgg acaccaacg tgtctgngaa aatcttgata 400
 gacatcatcg gactggactt tgcctttgca gaactctgtg ttgttccttt 450

gcggatcttc tccttcttcc cagttccagt cacagtgagg gcgcatctca 500

ccgggtggct gatgacactg aagaaaacct tcgtc 535

<210> 9

<211> 434

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> 32, 54, 80, 111, 117, 122, 139, 193, 205, 221, 226, 228, 273,
293, 296, 305, 336, 358, 361

<223> unknown base

<400> 9

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gttttggaca cccaaagtgt ttgagaaaat tttgatagac atnatcggag 200

tggantttgc ctttgcagaa ntttgnngtg ttccctttgcg gattttctcc 250

tttttcccag ttccagtcac agngagggcg catctcaccg ggnggntgat 300

gacantgaag aaaacctttg tccttgcccc cagctntttg gtgcggatca 350

ttgtcctnat ngccagcctt gtggctctac cctacctggg ggtgcacggt 400

gcgacctgg gcgtgggttc cctcctggcg ggca 434

<210> 10

<211> 154

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> 33, 49, 68, 83, 90, 98, 119

<223> unknown base

<400> 10

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acactgaaga aaaccttngt ccttgcccc agntttgtgn tgcggatnat 100

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agac 154

<210> 11

<211> 24

<212> DNA

<213> Artificial Sequence

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<220>
<223> Synthetic oligonucleotide probe

<400> 11
ctgatccggt tcttggtgcc cctg 24

<210> 12
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 12
gctctgtcac tcacgctc 18

<210> 13
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 13
tcattctcttc cctctccc 18

<210> 14
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 14
ccttccgccca cggagtgc 18

<210> 15
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 15
ggcaaagtcc actccgatga tgtc 24

<210> 16
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

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<400> 16
gcctgctgtg gtcacaggtc tccg 24

<210> 17

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 17

tcggggagca ggccttgaac cggggcattg ctgctgtcaa ggagg 45

<210> 18

<211> 1901

<212> DNA

<213> Homo sapiens

<400> 18

gccccgcgcc cggcgccggg cgcccgaagc cgggagccac cgccatgggg 50
gcctgcctgg gagcctgtc cctgtcagc tgcggtcct gcctctgcgg 100
ctctgcccc tgcatcctgt gcagctgctg ccccgccagc cgcaactcca 150
ccgtgagccg cctcatcttc acgttcttcc tcttcctggg ggtgctggtg 200
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 gcagggtggca gcctgtgagg gccgggcctt tgacaacgag caggacggcg 1200
 toacctacag ctactccttc ttccacttct gcctggtgct ggcctcactg 1250
 caggtcatga tgacgtcac caactggtac aagcccggtg agaccggaa 1300
 gatgatcagc acgtggaccg ccgtgtgggt gaagatctgt gccagctggg 1350
 cagggtgct cctctacctg tggaccctgg tagccccact cctcctgogc 1400
 aaccgcgact tcagctgagg cagcctcaca gcctgccatc tggtgccctc 1450
 tgccacctgg tgcctctcgg ctcggtgaca gccaacctgc cccctcccca 1500
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 ggggaactcc caccacagtg gggcatccgg cactgaagcc ctggtgttcc 1800
 tggtcacgtc cccagggga cctgcccc ttctggact tcgtgcctta 1850
 ctgagtctct aagacttttt ctaataaaca agccagtgcg tgtaaaaaaa 1900
 a 1901

<210> 19
 <211> 457
 <212> PRT
 <213> Homo sapiens

<400> 19
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 Cys Leu Cys Gly Ser Ala Pro Cys Ile Leu Cys Ser Cys Cys Pro
 20 25 30
 Ala Ser Arg Asn Ser Thr Val Ser Arg Leu Ile Phe Thr Phe Phe
 35 40 45
 Leu Phe Leu Gly Val Leu Val Ser Ile Ile Met Leu Ser Pro Gly
 50 55 60

Val	Glu	Ser	Gln	Leu	Tyr	Lys	Leu	Pro	Trp	Val	Cys	Glu	Glu	Gly		65	70	75
Ala	Gly	Ile	Pro	Thr	Val	Leu	Gln	Gly	His	Ile	Asp	Cys	Gly	Ser		80	85	90
Leu	Leu	Gly	Tyr	Arg	Ala	Val	Tyr	Arg	Met	Cys	Phe	Ala	Thr	Ala		95	100	105
Ala	Phe	Phe	Phe	Phe	Phe	Phe	Thr	Leu	Leu	Met	Leu	Cys	Val	Ser		110	115	120
Ser	Ser	Arg	Asp	Pro	Arg	Ala	Ala	Ile	Gln	Asn	Gly	Phe	Trp	Phe		125	130	135
Phe	Lys	Phe	Leu	Ile	Leu	Val	Gly	Leu	Thr	Val	Gly	Ala	Phe	Tyr		140	145	150
Ile	Pro	Asp	Gly	Ser	Phe	Thr	Asn	Ile	Trp	Phe	Tyr	Phe	Gly	Val		155	160	165
Val	Gly	Ser	Phe	Leu	Phe	Ile	Leu	Ile	Gln	Leu	Val	Leu	Leu	Ile		170	175	180
Asp	Phe	Ala	His	Ser	Trp	Asn	Gln	Arg	Trp	Leu	Gly	Lys	Ala	Glu		185	190	195
Glu	Cys	Asp	Ser	Arg	Ala	Trp	Tyr	Ala	Gly	Leu	Phe	Phe	Phe	Thr		200	205	210
Leu	Leu	Phe	Tyr	Leu	Leu	Ser	Ile	Ala	Ala	Val	Ala	Leu	Met	Phe		215	220	225
Met	Tyr	Tyr	Thr	Glu	Pro	Ser	Gly	Cys	His	Glu	Gly	Lys	Val	Phe		230	235	240
Ile	Ser	Leu	Asn	Leu	Thr	Phe	Cys	Val	Cys	Val	Ser	Ile	Ala	Ala		245	250	255
Val	Leu	Pro	Lys	Val	Gln	Asp	Ala	Gln	Pro	Asn	Ser	Gly	Leu	Leu		260	265	270
Gln	Ala	Ser	Val	Ile	Thr	Leu	Tyr	Thr	Met	Phe	Val	Thr	Trp	Ser		275	280	285
Ala	Leu	Ser	Ser	Ile	Pro	Glu	Gln	Lys	Cys	Asn	Pro	His	Leu	Pro		290	295	300
Thr	Gln	Leu	Gly	Asn	Glu	Thr	Val	Val	Ala	Gly	Pro	Glu	Gly	Tyr		305	310	315
Glu	Thr	Gln	Trp	Trp	Asp	Ala	Pro	Ser	Ile	Val	Gly	Leu	Ile	Ile		320	325	330
Phe	Leu	Leu	Cys	Thr	Leu	Phe	Ile	Ser	Leu	Arg	Ser	Ser	Asp	His		335	340	345
Arg	Gln	Val	Asn	Ser	Leu	Met	Gln	Thr	Glu	Glu	Cys	Pro	Pro	Met				

350	355	360
Leu Asp Ala Thr Gln Gln Gln Gln Gln Gln Val Ala Ala Cys Glu		
365	370	375
Gly Arg Ala Phe Asp Asn Glu Gln Asp Gly Val Thr Tyr Ser Tyr		
380	385	390
Ser Phe Phe His Phe Cys Leu Val Leu Ala Ser Leu His Val Met		
395	400	405
Met Thr Leu Thr Asn Trp Tyr Lys Pro Gly Glu Thr Arg Lys Met		
410	415	420
Ile Ser Thr Trp Thr Ala Val Trp Val Lys Ile Cys Ala Ser Trp		
425	430	435
Ala Gly Leu Leu Leu Tyr Leu Trp Thr Leu Val Ala Pro Leu Leu		
440	445	450
Leu Arg Asn Arg Asp Phe Ser		
455		

<210> 20
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 20
 gccgcctcat cttcacgttc ttcc 24

<210> 21
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 21
 tcatccagct ggtgctgctc 20

<210> 22
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 22
 cttcttccac ttctgcctgg 20

<210> 23
 <211> 18

<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 23
cctgggcaaa aatgcaac 18

<210> 24
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 24
caggaatgta gaaggcacc acgg 24

<210> 25
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 25
tggcacagat cttcacccac acgg 24

<210> 26
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 26
tgtccatcat tatgctgagc ccgggcgtgg agagtcagct ctacaagctg 50

<210> 27
<211> 1351
<212> DNA
<213> Homo sapiens

<400> 27
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ttaacctggg tcaaatgcac ggattctcac ctctacagt tacgtctctc 100
cgcggcacgt ccgcgaggac ttgaagtcct gagcgctcaa gtttgtccgt 150
aggtcgagag aaggccatgg aggtgccgcc accggcacog cggagctttc 200
tctgtagagc attgtgccta tttccccgag tctttgctgc cgaagctgtg 250

Asp	Ser	Glu	Val	Leu	Glu	Glu	Arg	Gln	Lys	Arg	Leu	Pro	Tyr	Val	35	40	45
Pro	Glu	Pro	Tyr	Tyr	Pro	Glu	Ser	Gly	Trp	Asp	Arg	Leu	Arg	Glu	50	55	60
Leu	Phe	Gly	Lys	Asp	Glu	Gln	Gln	Arg	Ile	Ser	Lys	Asp	Leu	Ala	65	70	75
Asn	Ile	Cys	Lys	Thr	Ala	Ala	Thr	Ala	Gly	Ile	Ile	Gly	Trp	Val	80	85	90
Tyr	Gly	Gly	Ile	Pro	Ala	Phe	Ile	His	Ala	Lys	Gln	Gln	Tyr	Ile	95	100	105
Glu	Gln	Ser	Gln	Ala	Glu	Ile	Tyr	His	Asn	Arg	Phe	Asp	Ala	Val	110	115	120
Gln	Ser	Ala	His	Arg	Ala	Ala	Thr	Arg	Gly	Phe	Ile	Arg	Tyr	Gly	125	130	135
Trp	Arg	Trp	Gly	Trp	Arg	Thr	Ala	Val	Phe	Val	Thr	Ile	Phe	Asn	140	145	150
Thr	Val	Asn	Thr	Ser	Leu	Asn	Val	Tyr	Arg	Asn	Lys	Asp	Ala	Leu	155	160	165
Ser	His	Phe	Val	Ile	Ala	Gly	Ala	Val	Thr	Gly	Ser	Leu	Phe	Arg	170	175	180
Ile	Asn	Val	Gly	Leu	Arg	Gly	Leu	Val	Ala	Gly	Gly	Ile	Ile	Gly	185	190	195
Ala	Leu	Leu	Gly	Thr	Pro	Val	Gly	Gly	Leu	Leu	Met	Ala	Phe	Gln	200	205	210
Lys	Tyr	Ala	Gly	Glu	Thr	Val	Gln	Glu	Arg	Lys	Gln	Lys	Asp	Arg	215	220	225
Lys	Ala	Leu	His	Glu	Leu	Lys	Leu	Glu	Glu	Trp	Lys	Gly	Arg	Leu	230	235	240
Gln	Val	Thr	Glu	His	Leu	Pro	Glu	Lys	Ile	Glu	Ser	Ser	Leu	Arg	245	250	255
Glu	Asp	Glu	Pro	Glu	Asn	Asp	Ala	Lys	Lys	Ile	Glu	Ala	Leu	Leu	260	265	270
Asn	Leu	Pro	Arg	Asn	Pro	Ser	Val	Ile	Asp	Lys	Gln	Asp	Lys	Asp	275	280	285

<210> 29

<211> 324

<212> DNA

<213> Homo sapiens

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 tgaacagcag agaatttcaa aggaccttgc taatatctgt aagacggcag 150
 ctacagcagg catcattggc tgggtgtatg ggggaatacc agcttttatt 200
 catgctaaac aacaatacat tgagcagagc caggcagaaa tttatcataa 250
 ccggtttgat gctgtgcaat ctgcacatcg tgctgccaca cgaggcttca 300
 ttcgttcatg gctggcgccg aacc 324

<210> 30
 <211> 377
 <212> DNA
 <213> Homo sapiens

<220>
 <221> unsure
 <222> 262, 330, 371
 <223> unknown base

<400> 30
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 gcggcttccc tacgtcccag agccctatta cccggaattt ggatgggacc 200
 gcctccggga gctgttttggc aaagatgaac agcagagaat ttcaaaggac 250
 cttgctgata tntgtaagac ggcagctaca gcaggcatca ttggctgggt 300
 gtatggggga ataccagctt ttattcatgn taaacaacaa tacattgagc 350
 agagccaggc agaaatttat nataacc 377

<210> 31
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 31
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<210> 32
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 32
cttgaggagc gtcagaagcg 20

<210> 33

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 33

ataacgaatg aagcctcgtg 20

<210> 34

<211> 40

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 34

gctaataatct gtaagacggc agctacagca ggcatcattg 40

<210> 35

<211> 1819

<212> DNA

<213> Homo sapiens

<400> 35

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gacaaagcag ctgtcaggga acctccgccg gagtogaatt tacgtgcagc 150
tgccgggaac cacagggttc aagatggttt gcgggggctt cgcgtgttcc 200
aagaactgcc tgtgcgccct caacctgctt tacaccttgg ttagtctgct 250
gctaattgga attgctgcgt ggggcattgg ctccgggctg atttccagtc 300
tccgagtggc cggcgtggc attgcagtgg gcatcttctt gttcctgatt 350
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cagttttaca gagatcctgg gtgtttggct gacctacaga tacaggaacc 750
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 agcactgtgc tgtgtagata gttcctactg gaaaaagagt ggaaatttat 1200
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 caattttttt tggctctttt aggaaagatt gttgtggtaa aaagtgttag 1300
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 aagtatatct atatgatctt gatattgttt tataataatt tgaagtctaa 1550
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 atctcccata atttgaaatt gaaatcgtat tgtgtggctc tgtatatctt 1750
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 taaaagaaag taatggaag 1819

<210> 36
 <211> 204
 <212> PRT
 <213> Homo sapiens

<400> 36
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 Leu Asn Leu Leu Tyr Thr Leu Val Ser Leu Leu Leu Ile Gly Ile
 20 25 30

Ala	Ala	Trp	Gly	Ile	Gly	Phe	Gly	Leu	Ile	Ser	Ser	Leu	Arg	Val	
				35					40					45	
Val	Gly	Val	Val	Ile	Ala	Val	Gly	Ile	Phe	Leu	Phe	Leu	Ile	Ala	
				50					55					60	
Leu	Val	Gly	Leu	Ile	Gly	Ala	Val	Lys	His	His	Gln	Val	Leu	Leu	
				65					70					75	
Phe	Phe	Tyr	Met	Ile	Ile	Leu	Leu	Leu	Val	Phe	Ile	Val	Gln	Phe	
				80					85					90	
Ser	Val	Ser	Cys	Ala	Cys	Leu	Ala	Leu	Asn	Gln	Glu	Gln	Gln	Gly	
				95					100					105	
Gln	Leu	Leu	Glu	Val	Gly	Trp	Asn	Asn	Thr	Ala	Ser	Ala	Arg	Asn	
				110					115					120	
Asp	Ile	Gln	Arg	Asn	Leu	Asn	Cys	Cys	Gly	Phe	Arg	Ser	Val	Asn	
				125					130					135	
Pro	Asn	Asp	Thr	Cys	Leu	Ala	Ser	Cys	Val	Lys	Ser	Asp	His	Ser	
				140					145					150	
Cys	Ser	Pro	Cys	Ala	Pro	Ile	Ile	Gly	Glu	Tyr	Ala	Gly	Glu	Val	
				155					160					165	
Leu	Arg	Phe	Val	Gly	Gly	Ile	Gly	Leu	Phe	Phe	Ser	Phe	Thr	Glu	
				170					175					180	
Ile	Leu	Gly	Val	Trp	Leu	Thr	Tyr	Arg	Tyr	Arg	Asn	Gln	Lys	Asp	
				185					190					195	
Pro	Arg	Ala	Asn	Pro	Ser	Ala	Phe	Leu							
				200											

<210> 37
 <211> 390
 <212> DNA
 <213> Homo sapiens

<220>
 <221> unsure
 <222> 20, 35, 61, 83, 106, 130, 133, 187, 232, 260, 336
 <223> unknown base

<400> 37
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 tattctgttaa nttgtattta ttgttcaggt ttntgtatct tgcgcttggt 100
 tagccontgaa ccaggagcaa cagggtcagn ttntggaggt tggttggaac 150
 aatacggcaa gtgctcgaaa tgacatccag agaaatntaa actgctgtgg 200
 gttccgaagt gttaacccaa atgacacctg tntggctagc tgtgttaaaa 250
 gtgaccactn gtgctcgcca tgtgctccaa tcataggaga atatgctgga 300

gaggttttga gatttggttg tggcattggc ctgttnttca gttttacaga 350
gatcctgggt gtttggtga cctacagata caggaaccag 390

<210> 38
<211> 566
<212> DNA
<213> Homo sapiens

<220>
<221> unsure
<222> 27
<223> unknown base

<400> 38
aatcccaaat tccccaattt ttttggnctt tttagggaaa gatgtgttgt 50
ggtaaaaaagt gttagtataa aaatgataat ttacttgtag tcttttatga 100
ttacaccaat gtattctaga atagttagt cttaggaaat tgtggtttaa 150
tttttgactt ttacaggtaa gtgcaaagga gaagtgggtt catgaaatgt 200
tctaattgat aataacattt accttcagcc tcccatcaga atggaacgag 250
ttttgagtaa tccaggaagt atatctatat gatcttgata ttgttttata 300
taatttgaag tctaaaagac tgcattttta aacaagttag tattaatgcg 350
ttggcccacg tagcaaaaag atatttgatt atcttaaaaa ttgttaaata 400
cogttttcat gaaagttctc agtattgtaa cagcaacttg tcaaacctaa 450
gcatatttga atatgatctc ccataatttg aaattgaaat cgtattgtgt 500
ggaggaaatg gcaatcttat gtgtgctgaa ggacacagta agagcaccaa 550
gttgtgcccc acttgc 566

<210> 39
<211> 264
<212> DNA
<213> Homo sapiens

<220>
<221> unsure
<222> 84-85, 206
<223> unknown base

<400> 39
atgattattc tggtacttgt atttattgtt cagttttatg gtatcttgcg 50
cttgtttagc ccctgaaacc aggagcaaca gggnnacagt tcttgagggt 100
tggttggtgcaa caatcacggc caagtgactc cgcaaatgac atcccagaga 150
aatcctaaac tgctgtgggt tccgaagtgt taacccaaat gacacctgtc 200

tggtctngctg tggtaaaaagt gaccactcgt gctcgccatg tgctccaatc 250

ataggagaat atgc 264

<210> 40

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 40

acccacgtct gcgttgctgc c 21

<210> 41

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 41

gagaatatgc tggagagg 18

<210> 42

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 42

aggaatgcac taggattcgc gcgg 24

<210> 43

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 43

ggccccaag gcaaggacaa agcagctgtc agggaaacctc cgccg 45

<210> 44

<211> 2061

<212> DNA

<213> Homo sapiens

<400> 44

cagtcacat gaagctgggc tgtgtcctca tggcctgggc cctctacctt 50

tcccttggtg tgctctgggt ggcccagatg ctactggctg ccagttttga 100

gacgctgcag tgtgagggac ctgtctgcac tgaggagagc agctgccaca 150
 cggaggatga cttgactgat gcaagggagc ctggcttcca ggtcaaggcc 200
 tacactttca gtgaaccctt ccacctgatt gtgtcctatg actggctgat 250
 cctccaaggc ccagccaagc cagtttttga aggggacctg ctggttctgc 300
 gctgccaggc ctggcaagac tggccactga ctcaggtgac cttctaccga 350
 gatggctcag ctctgggtcc ccccgggcct aacagggagt tctccatcac 400
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 agagccctgg tcctgggatc ccagaaacag catctgttgt ggctatcaca 500
 gtccaagaac tgtttccagc gccaatcttc agagctgtac cctcagctga 550
 accccaagca ggaagcccca tgaccctgag ttgtcagaca aagttgcccc 600
 tgcagaggtc agctgcccgc ctctcttctt ccttctacaa ggatggaagg 650
 atagtcaaaa gcagggggct ctctcagaa ttccagatcc ccacagcttc 700
 agaagatcac tccgggtcat actggtgtga ggcagccact gaggacaacc 750
 aagtttgga acagagcccc cagctagaga tcagagtga ggggtgcttc 800
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 tccaggaact gctcctgagg aggccctgg gcctctgct cgcgcgcaa 900
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 cctcatctgt atcaccagat gggccttctt ctcaaacaca tgcaggatgt 1000
 gagagtcttc ctcggtcacc tgctcatgga gttgagggaa ttatctggcc 1050
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 cttctgtcc tgcacatatg cataagtact tttacaagtt gtcccagtg 1200
 tttgttagaa taatgtagtt aggtgagtgt aaataaattt atataaagt 1250
 agaattagag tttagctata attgtgtatt ctctcttaac acaacagaat 1300
 tctgctgtct agatcaggaa tttctatctg ttatatogac cagaatgttg 1350
 tgatttaaag agaactaatg gaagtggatt gaatacagca gtctcaactg 1400
 ggggcaattt tgccccccag aggacattgg gcaatgtttg gagacatttt 1450
 ggtcattata cttggggggg tgggggatgg tgggatgtgt gtctactggc 1500
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ggcagtaccc cacaacgaaa aataatctgg cccaaaatgt cagttgtact 1600
gagtttgaga aaccccagcc taatgaaacc ctaggtgttg ggctctggaa 1650
tgggactttg tcccttctaa ttattatctc tttccagcct cattcagcta 1700
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tctagtttgt atcccctcaa aagccattat gttgaaatcc taatcccaa 1800
ggatgatggca ttaagaagtg ggcctttggg aagtgattag atcaggagtg 1850
cagagccctc atgattagga ttagtgcctt tatttaaaaa ggccccagag 1900
agctaactca cccttcacc atatgaggac gtggcaagaa gatgacatgt 1950
atgagaacca aaaaacagct gtcgccaaac accgactctg tcgttgccct 2000
gatcttgaac ttccagcctc cagaactatg agaaataaaa ttctggttgt 2050
ttgtagccta a 2061

<210> 45
<211> 359
<212> PRT
<213> Homo sapiens

<400> 45
Met Lys Leu Gly Cys Val Leu Met Ala Trp Ala Leu Tyr Leu Ser
1 5 10 15
Leu Gly Val Leu Trp Val Ala Gln Met Leu Leu Ala Ala Ser Phe
20 25 30
Glu Thr Leu Gln Cys Glu Gly Pro Val Cys Thr Glu Glu Ser Ser
35 40 45
Cys His Thr Glu Asp Asp Leu Thr Asp Ala Arg Glu Ala Gly Phe
50 55 60
Gln Val Lys Ala Tyr Thr Phe Ser Glu Pro Phe His Leu Ile Val
65 70 75
Ser Tyr Asp Trp Leu Ile Leu Gln Gly Pro Ala Lys Pro Val Phe
80 85 90
Glu Gly Asp Leu Leu Val Leu Arg Cys Gln Ala Trp Gln Asp Trp
95 100 105
Pro Leu Thr Gln Val Thr Phe Tyr Arg Asp Gly Ser Ala Leu Gly
110 115 120
Pro Pro Gly Pro Asn Arg Glu Phe Ser Ile Thr Val Val Gln Lys
125 130 135
Ala Asp Ser Gly His Tyr His Cys Ser Gly Ile Phe Gln Ser Pro
140 145 150

Gly	Pro	Gly	Ile	Pro	Glu	Thr	Ala	Ser	Val	Val	Ala	Ile	Thr	Val	155	160	165
Gln	Glu	Leu	Phe	Pro	Ala	Pro	Ile	Leu	Arg	Ala	Val	Pro	Ser	Ala	170	175	180
Glu	Pro	Gln	Ala	Gly	Ser	Pro	Met	Thr	Leu	Ser	Cys	Gln	Thr	Lys	185	190	195
Leu	Pro	Leu	Gln	Arg	Ser	Ala	Ala	Arg	Leu	Leu	Phe	Ser	Phe	Tyr	200	205	210
Lys	Asp	Gly	Arg	Ile	Val	Gln	Ser	Arg	Gly	Leu	Ser	Ser	Glu	Phe	215	220	225
Gln	Ile	Pro	Thr	Ala	Ser	Glu	Asp	His	Ser	Gly	Ser	Tyr	Trp	Cys	230	235	240
Glu	Ala	Ala	Thr	Glu	Asp	Asn	Gln	Val	Trp	Lys	Gln	Ser	Pro	Gln	245	250	255
Leu	Glu	Ile	Arg	Val	Gln	Gly	Ala	Ser	Ser	Ser	Ala	Ala	Pro	Pro	260	265	270
Thr	Leu	Asn	Pro	Ala	Pro	Gln	Lys	Ser	Ala	Ala	Pro	Gly	Thr	Ala	275	280	285
Pro	Glu	Glu	Ala	Pro	Gly	Pro	Leu	Pro	Pro	Pro	Pro	Thr	Pro	Ser	290	295	300
Ser	Glu	Asp	Pro	Gly	Phe	Ser	Ser	Pro	Leu	Gly	Met	Pro	Asp	Pro	305	310	315
His	Leu	Tyr	His	Gln	Met	Gly	Leu	Leu	Leu	Lys	His	Met	Gln	Asp	320	325	330
Val	Arg	Val	Leu	Leu	Gly	His	Leu	Leu	Met	Glu	Leu	Arg	Glu	Leu	335	340	345
Ser	Gly	His	Gln	Lys	Pro	Gly	Thr	Thr	Lys	Ala	Thr	Ala	Glu		350	355	

<210> 46

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 46

tgggctgtgt cctcatgg 18

<210> 47

<211> 18

<212> DNA

<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 47
tttccagcgc caattctc 18

<210> 48
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 48
agttcttgga ctgtgatagc cac 23

<210> 49
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 49
aaacttggtt gtcctcagtg gctg 24

<210> 50
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 50
gtgagggacc tgtctgcact gaggagagca gctgccacac ggagg 45

<210> 51
<211> 2181
<212> DNA
<213> Homo sapiens

<400> 51
cccacgcgtc cgcccacgcg tccgcccacg ggtccgcca cgcgccggg 50
ccaccagaag tttgagcctc tttggtagca ggaggctgga agaaaggaca 100
gaagtagctc tggctgtgat ggggatctta ctgggcctgc tactcctggg 150
gcacctaaaca gtggacaactt atggccgtcc catcctggaa gtgccagaga 200
gtgtaacagg accttggaag ggggatgtga atcttcctg cacctatgac 250
cccctgcaag gctacaccca agtcttggtg aagtggctgg tacaacgtgg 300
ctcagaccct gtcaccatct ttctacgtga ctcttctgga gaccatatcc 350

agcaggcaaa gtaccagggc cgcctgcatg tgagccacaa ggttccagga 400
 gatgtatccc tccaattgag caccctggag atggatgacc ggagccacta 450
 cacgtgtgaa gtcacctggc agactcctga tggcaaccaa gtcgtgagag 500
 ataagattac tgagctccgt gtccagaaac tctctgtctc caagcccaca 550
 gtgacaactg gcagcgggta tggcttcacg gtgccccagg gaatgaggat 600
 tagccttcaa tgccaggctc ggggttctcc tcccatcagt tatatttggg 650
 ataagcaaca gactaataac caggaaccca tcaaagtagc aaccctaagt 700
 accttactct tcaagcctgc ggtgatagcc gactcaggct cctatttctg 750
 cactgccaag ggccagggtg gctctgagca gcacagcgac attgtgaagt 800
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 acaaccatga cataccctt gaaagcaaca tctacagtga agcagtcctg 900
 ggactggacc actgacatgg atggctacct tggagagacc agtgctgggc 950
 caggaaagag cctgcctgtc tttgccatca tcctcatcat ctcttgtgc 1000
 tgtatggtgg tttttaccat ggcctatctc atgctctgtc ggaagacatc 1050
 ccaacaagag catgtctacg aagcagccag gtaagaaagt ctctcctctt 1100
 ccatttttga ccccgctcct gccctcaatt ttgattactg gcaggaaatg 1150
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 agggtcagga catagctgcc ttccctctct caggcacctt ctgaggttgt 1250
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 ccagaatccc tgggtggtag gatcctgata attaattggc aagaattgag 1350
 gcagaagggg gggaaaccag gaccacagcc ccaagtcctt tcttatgggt 1400
 ggtgggctct tgggcatag ggcacatgcc agagaggcca acgactctgg 1450
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 caacttccca gaatctgggc aacaactact ctgatgagcc ctgcatagga 1550
 caggagtacc agatcatcgc ccagatcaat ggcaactacg cccgcctgct 1600
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ctttgccctg gaatttgcca gatgcatctc aagtaagcca gctgctggat 1850
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 tctaaatacc agaggggaaga tgcccatagc actaggactt ggtcatcatg 1950
 cctacagaca ctattcaact ttggcatctt gccaccagaa gacccgaggg 2000
 aggctcagct ctgccagctc agaggaccag ctatatccag gatcatttct 2050
 ctttcttcag ggccagacag cttttaattg aaattgttat ttcacaggcc 2100
 agggttcagt tctgctcctc cactataagt ctaatgttct gactctctcc 2150
 tggtgctcaa taaatatcta atcataacag c 2181

<210> 52
 <211> 321
 <212> PRT
 <213> Homo sapiens

<400> 52
 Met Gly Ile Leu Leu Gly Leu Leu Leu Leu Gly His Leu Thr Val
 1 5 10 15
 Asp Thr Tyr Gly Arg Pro Ile Leu Glu Val Pro Glu Ser Val Thr
 20 25 30
 Gly Pro Trp Lys Gly Asp Val Asn Leu Pro Cys Thr Tyr Asp Pro
 35 40 45
 Leu Gln Gly Tyr Thr Gln Val Leu Val Lys Trp Leu Val Gln Arg
 50 55 60
 Gly Ser Asp Pro Val Thr Ile Phe Leu Arg Asp Ser Ser Gly Asp
 65 70 75
 His Ile Gln Gln Ala Lys Tyr Gln Gly Arg Leu His Val Ser His
 80 85 90
 Lys Val Pro Gly Asp Val Ser Leu Gln Leu Ser Thr Leu Glu Met
 95 100 105
 Asp Asp Arg Ser His Tyr Thr Cys Glu Val Thr Trp Gln Thr Pro
 110 115 120
 Asp Gly Asn Gln Val Val Arg Asp Lys Ile Thr Glu Leu Arg Val
 125 130 135
 Gln Lys Leu Ser Val Ser Lys Pro Thr Val Thr Thr Gly Ser Gly
 140 145 150
 Tyr Gly Phe Thr Val Pro Gln Gly Met Arg Ile Ser Leu Gln Cys
 155 160 165
 Gln Ala Arg Gly Ser Pro Pro Ile Ser Tyr Ile Trp Tyr Lys Gln
 170 175 180

Gln	Thr	Asn	Asn	Gln	Glu	Pro	Ile	Lys	Val	Ala	Thr	Leu	Ser	Thr	
				185					190					195	
Leu	Leu	Phe	Lys	Pro	Ala	Val	Ile	Ala	Asp	Ser	Gly	Ser	Tyr	Phe	
				200					205					210	
Cys	Thr	Ala	Lys	Gly	Gln	Val	Gly	Ser	Glu	Gln	His	Ser	Asp	Ile	
				215					220					225	
Val	Lys	Phe	Val	Val	Lys	Asp	Ser	Ser	Lys	Leu	Leu	Lys	Thr	Lys	
				230					235					240	
Thr	Glu	Ala	Pro	Thr	Thr	Met	Thr	Tyr	Pro	Leu	Lys	Ala	Thr	Ser	
				245					250					255	
Thr	Val	Lys	Gln	Ser	Trp	Asp	Trp	Thr	Thr	Asp	Met	Asp	Gly	Tyr	
				260					265					270	
Leu	Gly	Glu	Thr	Ser	Ala	Gly	Pro	Gly	Lys	Ser	Leu	Pro	Val	Phe	
				275					280					285	
Ala	Ile	Ile	Leu	Ile	Ile	Ser	Leu	Cys	Cys	Met	Val	Val	Phe	Thr	
				290					295					300	
Met	Ala	Tyr	Ile	Met	Leu	Cys	Arg	Lys	Thr	Ser	Gln	Gln	Glu	His	
				305					310					315	
Val	Tyr	Glu	Ala	Ala	Arg										
				320											

<210> 53

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 53

tatccctcca attgagcacc ctgg 24

<210> 54

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 54

gtcggaagac atcccaacaa g 21

<210> 55

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 55

cttcacaatg tcgctgtgct gctc 24

<210> 56

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 56

agccaaatcc agcagctggc ttac 24

<210> 57

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 57

tgcatgaccg gagccactac acgtgtgaag tcacctggca gactoctgat 50

<210> 58

<211> 2458

<212> DNA

<213> Homo sapiens

<400> 58

gcgcggggag cccatctgcc ccagggggca cggggcgcg ggccggctcc 50

cgccccggcac atggctgcag ccacctcgcg cgcaccccgga ggccggcgcg 100

ccagctcgcc cgaggtccgt cggaggcgcc cggccgcccc ggagccaagc 150

agcaactgag cggggaagcg cccgcgtccg gggatcgga tgccctctct 200

ccttctctctc ttgctagttt cctactatgt tggaaccttg gggactcaca 250

ctgagatcaa gagagtggca gaggaaaagg tcactttgcc ctgccaccat 300

caactggggc ttccagaaaa agacactctg gatattgaat ggctgctcac 350

cgataatgaa gggaaccaa aagtggatgat cacttactcc agtcgtcatg 400

tctacaataa cttgactgag gaacagaagg gccgagtggc ctttgcttcc 450

aatttctctgg caggagatgc ctcttgtag attgaacctc tgaagcccag 500

tgatgagggc cggtagacct gtaagggtta gaattcaggg cgctacgtgt 550

ggagccatgt catcttaaaa gtcttagtga gaccatccaa gcccaagtgt 600

gagttggaag gagagctgac agaaggaagt gacctgactt tgcagtgtga 650

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 aaccaccctg gacgagttct gctgcagaat cttaccatgt cctactctgg 800
 actgtaccag tgcacagcag gcaacgaagc tgggaaggaa agctgtgtgg 850
 tgcgagtaac tgtacagtat gtacaaagca tcggcatggg tgcaggagca 900
 gtgacaggca tagtggctgg agccctgctg attttcctct tgggtgtggct 950
 gctaatacga aggaaagaca aagaaagata tgaggaagaa gagagaccta 1000
 atgaaattcg agaagatgct gaagctccaa aagcccgtct tgtgaaacct 1050
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 acgcagcacc ccagccaggg ctggccaccc aggcatacag cctagtgggg 1200
 ccagaggtga gaggttctga accaaagaaa gtccaccatg ctaatctgac 1250
 caaagcagaa accacaccca gcatgatccc cagccagagc agagccttcc 1300
 aaacgggtctg aattacaatg gacttgactc ccacgctttc ctaggagtca 1350
 ggggtctttg actcttctcg tcattggagc tcaagtcacc agccacacaa 1400
 ccagatgaga ggtcatctaa gtagcagtga gcattgcacg gaacagattc 1450
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 gattcatctg taaaaaggca tcttattgtg ccttttagacc agagtaaggg 1550
 aaagcaggag tccaaatcta tttgttgacc aggacctgtg gtgagaagggt 1600
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 gtatcagtgc tttgattcac aattttcaag aggaaatggg atgctgtttg 1700
 taaattttct atgcatttct gcaaacttat tggattatta gttattcaga 1750
 cagtcaagca gaaccacag cttattaca cctgtctaca ccattgtactg 1800
 agctaaccac ttctaagaaa ctccaaaaaa ggaaacatgt gtcttctatt 1850
 ctgacttaac ttcatttgc ataaggtttg gatattaatt tcaaggggag 1900
 ttgaaatagt gggagatgga gaagagtga tgagtttctc ccactctata 1950
 ctaatctcac tatttgtatt gagcccaaaa taactatgaa aggagacaaa 2000
 aatttgtgac aaaggattgt gaagagcttt ccatcttcat gatgttatga 2050
 ggattgttga caaacattag aaatatataa tggagcaatt gtggatttcc 2100

cctcaaatca gatgcctcta aggactttcc tgctagatat ttctggaagg 2150
 agaaaataca acatgtcatt tatcaacgtc cttagaaaga attcttctag 2200
 agaaaaaggg atctaggaat gctgaaagat taccacaacat accattatag 2250
 tctcttcttt ctgagaaaat gtgaaaccag aattgcaaga ctgggtggac 2300
 tagaaagga gattagatca gttttctctt aatatgtcaa ggaaggtagc 2350
 cgggcatggt gccaggcacc tgtaggaaaa tccagcaggt ggaggttgca 2400
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 <211> 373
 <212> PRT
 <213> Homo sapiens

<400> 59
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 35 40 45
 Thr Leu Asp Ile Glu Trp Leu Leu Thr Asp Asn Glu Gly Asn Gln
 50 55 60
 Lys Val Val Ile Thr Tyr Ser Ser Arg His Val Tyr Asn Asn Leu
 65 70 75
 Thr Glu Glu Gln Lys Gly Arg Val Ala Phe Ala Ser Asn Phe Leu
 80 85 90
 Ala Gly Asp Ala Ser Leu Gln Ile Glu Pro Leu Lys Pro Ser Asp
 95 100 105
 Glu Gly Arg Tyr Thr Cys Lys Val Lys Asn Ser Gly Arg Tyr Val
 110 115 120
 Trp Ser His Val Ile Leu Lys Val Leu Val Arg Pro Ser Lys Pro
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 Lys Cys Glu Leu Glu Gly Glu Leu Thr Glu Gly Ser Asp Leu Thr
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 Leu Gln Cys Glu Ser Ser Ser Gly Thr Glu Pro Ile Val Tyr Tyr
 155 160 165
 Trp Gln Arg Ile Arg Glu Lys Glu Gly Glu Asp Glu Arg Leu Pro
 170 175 180

Pro	Lys	Ser	Arg	Ile	Asp	Tyr	Asn	His	Pro	Gly	Arg	Val	Leu	Leu	185	190	195
Gln	Asn	Leu	Thr	Met	Ser	Tyr	Ser	Gly	Leu	Tyr	Gln	Cys	Thr	Ala	200	205	210
Gly	Asn	Glu	Ala	Gly	Lys	Glu	Ser	Cys	Val	Val	Arg	Val	Thr	Val	215	220	225
Gln	Tyr	Val	Gln	Ser	Ile	Gly	Met	Val	Ala	Gly	Ala	Val	Thr	Gly	230	235	240
Ile	Val	Ala	Gly	Ala	Leu	Leu	Ile	Phe	Leu	Leu	Val	Trp	Leu	Leu	245	250	255
Ile	Arg	Arg	Lys	Asp	Lys	Glu	Arg	Tyr	Glu	Glu	Glu	Glu	Arg	Pro	260	265	270
Asn	Glu	Ile	Arg	Glu	Asp	Ala	Glu	Ala	Pro	Lys	Ala	Arg	Leu	Val	275	280	285
Lys	Pro	Ser	Ser	Ser	Ser	Ser	Gly	Ser	Arg	Ser	Ser	Arg	Ser	Gly	290	295	300
Ser	Ser	Ser	Thr	Arg	Ser	Thr	Ala	Asn	Ser	Ala	Ser	Arg	Ser	Gln	305	310	315
Arg	Thr	Leu	Ser	Thr	Asp	Ala	Ala	Pro	Gln	Pro	Gly	Leu	Ala	Thr	320	325	330
Gln	Ala	Tyr	Ser	Leu	Val	Gly	Pro	Glu	Val	Arg	Gly	Ser	Glu	Pro	335	340	345
Lys	Lys	Val	His	His	Ala	Asn	Leu	Thr	Lys	Ala	Glu	Thr	Thr	Pro	350	355	360
Ser	Met	Ile	Pro	Ser	Gln	Ser	Arg	Ala	Phe	Gln	Thr	Val			365	370	

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<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 60

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<210> 61

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 61
actaggctgt atgcctgggt gggc 24

<210> 62

<211> 43

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 62

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<210> 63

<211> 3534

<212> DNA

<213> Homo sapiens

<400> 63

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<210> 64
 <211> 655
 <212> PRT
 <213> Homo sapiens

<400> 64
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 Arg Ile Ala Arg Arg Ala Thr Ala Thr Met Ile Ala Gly Ser Leu
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Leu	Leu	Leu	Gly	Phe	Leu	Ser	Thr	Thr	Thr	Ala	Gln	Pro	Glu	Gln	35	40	45
Lys	Ala	Ser	Asn	Leu	Ile	Gly	Thr	Tyr	Arg	His	Val	Asp	Arg	Ala	50	55	60
Thr	Gly	Gln	Val	Leu	Thr	Cys	Asp	Lys	Cys	Pro	Ala	Gly	Thr	Tyr	65	70	75
Val	Ser	Glu	His	Cys	Thr	Asn	Thr	Ser	Leu	Arg	Val	Cys	Ser	Ser	80	85	90
Cys	Pro	Val	Gly	Thr	Phe	Thr	Arg	His	Glu	Asn	Gly	Ile	Glu	Lys	95	100	105
Cys	His	Asp	Cys	Ser	Gln	Pro	Cys	Pro	Trp	Pro	Met	Ile	Glu	Lys	110	115	120
Leu	Pro	Cys	Ala	Ala	Leu	Thr	Asp	Arg	Glu	Cys	Thr	Cys	Pro	Pro	125	130	135
Gly	Met	Phe	Gln	Ser	Asn	Ala	Thr	Cys	Ala	Pro	His	Thr	Val	Cys	140	145	150
Pro	Val	Gly	Trp	Gly	Val	Arg	Lys	Lys	Gly	Thr	Glu	Thr	Glu	Asp	155	160	165
Val	Arg	Cys	Lys	Gln	Cys	Ala	Arg	Gly	Thr	Phe	Ser	Asp	Val	Pro	170	175	180
Ser	Ser	Val	Met	Lys	Cys	Lys	Ala	Tyr	Thr	Asp	Cys	Leu	Ser	Gln	185	190	195
Asn	Leu	Val	Val	Ile	Lys	Pro	Gly	Thr	Lys	Glu	Thr	Asp	Asn	Val	200	205	210
Cys	Gly	Thr	Leu	Pro	Ser	Phe	Ser	Ser	Ser	Thr	Ser	Pro	Ser	Pro	215	220	225
Gly	Thr	Ala	Ile	Phe	Pro	Arg	Pro	Glu	His	Met	Glu	Thr	His	Glu	230	235	240
Val	Pro	Ser	Ser	Thr	Tyr	Val	Pro	Lys	Gly	Met	Asn	Ser	Thr	Glu	245	250	255
Ser	Asn	Ser	Ser	Ala	Ser	Val	Arg	Pro	Lys	Val	Leu	Ser	Ser	Ile	260	265	270
Gln	Glu	Gly	Thr	Val	Pro	Asp	Asn	Thr	Ser	Ser	Ala	Arg	Gly	Lys	275	280	285
Glu	Asp	Val	Asn	Lys	Thr	Leu	Pro	Asn	Leu	Gln	Val	Val	Asn	His	290	295	300
Gln	Gln	Gly	Pro	His	His	Arg	His	Ile	Leu	Lys	Leu	Leu	Pro	Ser	305	310	315
Met	Glu	Ala	Thr	Gly	Gly	Glu	Lys	Ser	Ser	Thr	Pro	Ile	Lys	Gly			

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Pro Lys Arg Gly His	Pro Arg Gln Asn Leu His Lys His Phe Asp	
335	340	345
Ile Asn Glu His Leu	Pro Trp Met Ile Val Leu Phe Leu Leu Leu	
350	355	360
Val Leu Val Val Ile	Val Val Cys Ser Ile Arg Lys Ser Ser Arg	
365	370	375
Thr Leu Lys Lys Gly	Pro Arg Gln Asp Pro Ser Ala Ile Val Glu	
380	385	390
Lys Ala Gly Leu Lys	Lys Ser Met Thr Pro Thr Gln Asn Arg Glu	
395	400	405
Lys Trp Ile Tyr Tyr	Cys Asn Gly His Gly Ile Asp Ile Leu Lys	
410	415	420
Leu Val Ala Ala Gln	Val Gly Ser Gln Trp Lys Asp Ile Tyr Gln	
425	430	435
Phe Leu Cys Asn Ala	Ser Glu Arg Glu Val Ala Ala Phe Ser Asn	
440	445	450
Gly Tyr Thr Ala Asp	His Glu Arg Ala Tyr Ala Ala Leu Gln His	
455	460	465
Trp Thr Ile Arg Gly	Pro Glu Ala Ser Leu Ala Gln Leu Ile Ser	
470	475	480
Ala Leu Arg Gln His	Arg Arg Asn Asp Val Val Glu Lys Ile Arg	
485	490	495
Gly Leu Met Glu Asp	Thr Thr Gln Leu Glu Thr Asp Lys Leu Ala	
500	505	510
Leu Pro Met Ser Pro	Ser Pro Leu Ser Pro Ser Pro Ile Pro Ser	
515	520	525
Pro Asn Ala Lys Leu	Glu Asn Ser Ala Leu Leu Thr Val Glu Pro	
530	535	540
Ser Pro Gln Asp Lys	Asn Lys Gly Phe Phe Val Asp Glu Ser Glu	
545	550	555
Pro Leu Leu Arg Cys	Asp Ser Thr Ser Ser Gly Ser Ser Ala Leu	
560	565	570
Ser Arg Asn Gly Ser	Phe Ile Thr Lys Glu Lys Lys Asp Thr Val	
575	580	585
Leu Arg Gln Val Arg	Leu Asp Pro Cys Asp Leu Gln Pro Ile Phe	
590	595	600
Asp Asp Met Leu His	Phe Leu Asn Pro Glu Glu Leu Arg Val Ile	
605	610	615

Glu	Glu	Ile	Pro	Gln	Ala	Glu	Asp	Lys	Leu	Asp	Arg	Leu	Phe	Glu
				620					625					630
Ile	Ile	Gly	Val	Lys	Ser	Gln	Glu	Ala	Ser	Gln	Thr	Leu	Leu	Asp
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Ser	Val	Tyr	Ser	His	Leu	Pro	Asp	Leu	Leu					
				650					655					

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<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 65

gtagcagtgc acatggggtg ttgg 24

<210> 66

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 66

accgcacatc ctcagtctct gtcc 24

<210> 67

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 67

acgatgatcg cgggctccct tctcctgctt ggattcotta gcaccaccac 50

<210> 68

<211> 2412

<212> DNA

<213> Homo sapiens

<400> 68

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acatttttgg gactcgggaa ttatgaggta gaggtggagg cggagccgga 100

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ttgaagcccc cttctcattc cgatcgcttt ttggccttga tgatttgaaa 200

ataagtctg ttgcaccaga tgcagatgct gttgctgcac agatcctgtc 250

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<210> 69
 <211> 453
 <212> PRT
 <213> Homo sapiens

<400> 69
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 Pro Asp Ala Asp Ala Val Ala Ala Gln Ile Leu Ser Leu Leu Pro
 35 40 45
 Leu Lys Phe Phe Pro Ile Ile Val Ile Gly Ile Ile Ala Leu Ile
 50 55 60
 Leu Ala Leu Ala Ile Gly Leu Gly Ile His Phe Asp Cys Ser Gly
 65 70 75
 Lys Tyr Arg Cys Arg Ser Ser Phe Lys Cys Ile Glu Leu Ile Ala
 80 85 90
 Arg Cys Asp Gly Val Ser Asp Cys Lys Asp Gly Glu Asp Glu Tyr
 95 100 105
 Arg Cys Val Arg Val Gly Gly Gln Asn Ala Val Leu Gln Val Phe

110					115					120				
Thr	Ala	Ala	Ser	Trp	Lys	Thr	Met	Cys	Ser	Asp	Asp	Trp	Lys	Gly
				125					130					135
His	Tyr	Ala	Asn	Val	Ala	Cys	Ala	Gln	Leu	Gly	Phe	Pro	Ser	Tyr
				140					145					150
Val	Ser	Ser	Asp	Asn	Leu	Arg	Val	Ser	Ser	Leu	Glu	Gly	Gln	Phe
				155					160					165
Arg	Glu	Glu	Phe	Val	Ser	Ile	Asp	His	Leu	Leu	Pro	Asp	Asp	Lys
				170					175					180
Val	Thr	Ala	Leu	His	His	Ser	Val	Tyr	Val	Arg	Glu	Gly	Cys	Ala
				185					190					195
Ser	Gly	His	Val	Val	Thr	Leu	Gln	Cys	Thr	Ala	Cys	Gly	His	Arg
				200					205					210
Arg	Gly	Tyr	Ser	Ser	Arg	Ile	Val	Gly	Gly	Asn	Met	Ser	Leu	Leu
				215					220					225
Ser	Gln	Trp	Pro	Trp	Gln	Ala	Ser	Leu	Gln	Phe	Gln	Gly	Tyr	His
				230					235					240
Leu	Cys	Gly	Gly	Ser	Val	Ile	Thr	Pro	Leu	Trp	Ile	Ile	Thr	Ala
				245					250					255
Ala	His	Cys	Val	Tyr	Asp	Leu	Tyr	Leu	Pro	Lys	Ser	Trp	Thr	Ile
				260					265					270
Gln	Val	Gly	Leu	Val	Ser	Leu	Leu	Asp	Asn	Pro	Ala	Pro	Ser	His
				275					280					285
Leu	Val	Glu	Lys	Ile	Val	Tyr	His	Ser	Lys	Tyr	Lys	Pro	Lys	Arg
				290					295					300
Leu	Gly	Asn	Asp	Ile	Ala	Leu	Met	Lys	Leu	Ala	Gly	Pro	Leu	Thr
				305					310					315
Phe	Asn	Glu	Met	Ile	Gln	Pro	Val	Cys	Leu	Pro	Asn	Ser	Glu	Glu
				320					325					330
Asn	Phe	Pro	Asp	Gly	Lys	Val	Cys	Trp	Thr	Ser	Gly	Trp	Gly	Ala
				335					340					345
Thr	Glu	Asp	Gly	Gly	Asp	Ala	Ser	Pro	Val	Leu	Asn	His	Ala	Ala
				350					355					360
Val	Pro	Leu	Ile	Ser	Asn	Lys	Ile	Cys	Asn	His	Arg	Asp	Val	Tyr
				365					370					375
Gly	Gly	Ile	Ile	Ser	Pro	Ser	Met	Leu	Cys	Ala	Gly	Tyr	Leu	Thr
				380					385					390
Gly	Gly	Val	Asp	Ser	Cys	Gln	Gly	Asp	Ser	Gly	Gly	Pro	Leu	Val
				395					400					405

Cys Gln Glu Arg Arg Leu Trp Lys Leu Val Gly Ala Thr Ser Phe
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Gly Ile Gly Cys Ala Glu Val Asn Lys Pro Gly Val Tyr Thr Arg
425 430 435

Val Thr Ser Phe Leu Asp Trp Ile His Glu Gln Met Glu Arg Asp
440 445 450

Leu Lys Thr

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<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 70
tgacatcgcc cttatgaagc tggc 24

<210> 71
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 71
tacacgtccc tgtggttgca gatc 24

<210> 72
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 72
cgttcaatgc agaaatgatc cagcctgtgt gcctgcccac ctctgaagag 50

<210> 73
<211> 3305
<212> DNA
<213> Homo sapiens

<400> 73
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tccatocaag caaactgaat ggcaatgaaa caaactggag aagaaggtag 3100

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 caacccttca ttttaacaagt aagaatgtta aaaagtgaaa acaatgtaag 3250
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 gaaat 3305

<210> 74
 <211> 735
 <212> PRT
 <213> Homo sapiens

<400> 74
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 Val Ser Leu Trp Asn Gln Gly Arg Ala Asp Glu Val Val Ser Ala
 35 40 45
 Ser Val Arg Ser Gly Asp Leu Trp Ile Pro Val Lys Ser Phe Asp
 50 55 60
 Ser Lys Asn His Pro Glu Val Leu Asn Ile Arg Leu Gln Arg Glu
 65 70 75
 Ser Lys Glu Leu Ile Ile Asn Leu Glu Arg Asn Glu Gly Leu Ile
 80 85 90
 Ala Ser Ser Phe Thr Glu Thr His Tyr Leu Gln Asp Gly Thr Asp
 95 100 105
 Val Ser Leu Ala Arg Asn Tyr Thr Gly His Cys Tyr Tyr His Gly
 110 115 120
 His Val Arg Gly Tyr Ser Asp Ser Ala Val Ser Leu Ser Thr Cys
 125 130 135
 Ser Gly Leu Arg Gly Leu Ile Val Phe Glu Asn Glu Ser Tyr Val
 140 145 150
 Leu Glu Pro Met Lys Ser Ala Thr Asn Arg Tyr Lys Leu Phe Pro
 155 160 165
 Ala Lys Lys Leu Lys Ser Val Arg Gly Ser Cys Gly Ser His His
 170 175 180
 Asn Thr Pro Asn Leu Ala Ala Lys Asn Val Phe Pro Pro Pro Ser
 185 190 195
 Gln Thr Trp Ala Arg Arg His Lys Arg Glu Thr Leu Lys Ala Thr
 200 205 210

Lys Tyr Val Glu	Leu Val Ile Val Ala	Asp Asn Arg Glu Phe Gln	215	220	225
Arg Gln Gly Lys	Asp Leu Glu Lys Val	Lys Gln Arg Leu Ile Glu	230	235	240
Ile Ala Asn His	Val Asp Lys Phe Tyr	Arg Pro Leu Asn Ile Arg	245	250	255
Ile Val Leu Val	Gly Val Glu Val Trp	Asn Asp Met Asp Lys Cys	260	265	270
Ser Val Ser Gln	Asp Pro Phe Thr Ser	Leu His Glu Phe Leu Asp	275	280	285
Trp Arg Lys Met	Lys Leu Leu Pro Arg	Lys Ser His Asp Asn Ala	290	295	300
Gln Leu Val Ser	Gly Val Tyr Phe Gln	Gly Thr Thr Ile Gly Met	305	310	315
Ala Pro Ile Met	Ser Met Cys Thr Ala	Asp Gln Ser Gly Gly Ile	320	325	330
Val Met Asp His	Ser Asp Asn Pro Leu	Gly Ala Ala Val Thr Leu	335	340	345
Ala His Glu Leu	Gly His Asn Phe Gly	Met Asn His Asp Thr Leu	350	355	360
Asp Arg Gly Cys	Ser Cys Gln Met Ala	Val Glu Lys Gly Gly Cys	365	370	375
Ile Met Asn Ala	Ser Thr Gly Tyr Pro	Phe Pro Met Val Phe Ser	380	385	390
Ser Cys Ser Arg	Lys Asp Leu Glu Thr	Ser Leu Glu Lys Gly Met	395	400	405
Gly Val Cys Leu	Phe Asn Leu Pro Glu	Val Arg Glu Ser Phe Gly	410	415	420
Gly Gln Lys Cys	Gly Asn Arg Phe Val	Glu Glu Gly Glu Glu Cys	425	430	435
Asp Cys Gly Glu	Pro Glu Glu Cys Met	Asn Arg Cys Cys Asn Ala	440	445	450
Thr Thr Cys Thr	Leu Lys Pro Asp Ala	Val Cys Ala His Gly Leu	455	460	465
Cys Cys Glu Asp	Cys Gln Leu Lys Pro	Ala Gly Thr Ala Cys Arg	470	475	480
Asp Ser Ser Asn	Ser Cys Asp Leu Pro	Glu Phe Cys Thr Gly Ala	485	490	495
Ser Pro His Cys	Pro Ala Asn Val Tyr	Leu His Asp Gly His Ser			

500	505	510
Cys Gln Asp Val Asp Gly Tyr Cys Tyr	Asn Gly Ile Cys Gln Thr	
515	520	525
His Glu Gln Gln Cys Val Thr Leu Trp	Gly Pro Gly Ala Lys Pro	
530	535	540
Ala Pro Gly Ile Cys Phe Glu Arg Val	Asn Ser Ala Gly Asp Pro	
545	550	555
Tyr Gly Asn Cys Gly Lys Val Ser Lys	Ser Ser Phe Ala Lys Cys	
560	565	570
Glu Met Arg Asp Ala Lys Cys Gly Lys	Ile Gln Cys Gln Gly Gly	
575	580	585
Ala Ser Arg Pro Val Ile Gly Thr Asn	Ala Val Ser Ile Glu Thr	
590	595	600
Asn Ile Pro Leu Gln Gln Gly Gly Arg	Ile Leu Cys Arg Gly Thr	
605	610	615
His Val Tyr Leu Gly Asp Asp Met Pro	Asp Pro Gly Leu Val Leu	
620	625	630
Ala Gly Thr Lys Cys Ala Asp Gly Lys	Ile Cys Leu Asn Arg Gln	
635	640	645
Cys Gln Asn Ile Ser Val Phe Gly Val	His Glu Cys Ala Met Gln	
650	655	660
Cys His Gly Arg Gly Val Cys Asn Asn	Arg Lys Asn Cys His Cys	
665	670	675
Glu Ala His Trp Ala Pro Pro Phe Cys	Asp Lys Phe Gly Phe Gly	
680	685	690
Gly Ser Thr Asp Ser Gly Pro Ile Arg	Gln Ala Glu Ala Arg Gln	
695	700	705
Glu Ala Ala Glu Ser Asn Arg Glu Arg	Gly Gln Gly Gln Glu Pro	
710	715	720
Val Gly Ser Gln Glu His Ala Ser Thr	Ala Ser Leu Thr Leu Ile	
725	730	735

<210> 75
 <211> 483
 <212> DNA
 <213> Homo sapiens

 <220>
 <221> unsure
 <222> 30, 94, 143, 156, 163, 179, 193, 369, 371, 381, 390, 473
 <223> unknown base

 <400> 75

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 ctgacaacga aaacaaaaca gttttggggg ttcaggaggg gaantccagc 100
 ctaccaggga agtttgaga aacagtgcaa ggaagggcag ganttcctgg 150
 ttgagntttt tgntaaaaca tggacatgnt tcagtgtctgc tcntgagaga 200
 gtagcagggtt accacttttg gcaggcccca gccctgcagc aaggagggaag 250
 aggactcaaa agtttggcct ttcactgagc ctccacagca gtggggggaga 300
 agcaagggtt gggcccagtg tcccctttcc ccagtgcac ctcagccttg 350
 gcagccctga taactggtnt ntggctgcaa nttaatgctn tgatatggct 400
 tttagcattt attatatgaa aatagcaggg ttttagtttt taatttatca 450
 gagaccctgc caccattcc atntccatcc aag 483

<210> 76
 <211> 27
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic oligonucleotide probe

<400> 76
 gtctcagcac gtgttctggt ctcaggg 27

<210> 77
 <211> 18
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic oligonucleotide probe

<400> 77
 catgagcatg tgcacggc 18

<210> 78
 <211> 18
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic oligonucleotide probe

<400> 78
 tacctgcacg atgggcac 18

<210> 79
 <211> 18
 <212> DNA
 <213> Artificial Sequence

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 atgatctgcc cgctcggcc tcccaaagtg ctgggattac aggcgagtgc 150
 aaccacaccc ggccacaaac tttttaagaa gttaatgaaa ccataccttt 200
 tacattttta atgacaggaa aatgctcaca ataattgtta acccaaaatt 250
 ctggatacaa aagtacaatc ttactgtgt aaatacatgt atatgtacta 300
 tatgaaaata taccaaatat caataatact tatctctggg taaaaacctc 350
 ttctcatacc ctgtgctaac aacttttaac aaaaaatttg catcactttt 400
 aagaatcaag aaaaatttct gaaggtcata tgggacagaa aaaaaacca 450
 agggaaaaat cagccactt gggaaaaaa gattcgaaat ctgccttttt 500
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<210> 85
<211> 67
<212> PRT
<213> Homo sapiens

<400> 85
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Leu Ala Leu Leu Leu Pro Val Gln Val Ser Ser Phe Val Pro Leu
20 25 30
Thr Ser Met Pro Glu Ala Thr Ala Ala Glu Thr Thr Lys Pro Ser
35 40 45
Asn Ser Ala Leu Gln Pro Thr Ala Gly Leu Leu Val Val Leu Leu
50 55 60
Ala Leu Leu His Leu Tyr His
65

<210> 86
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 86
acgggcacac tggatcccaa atg 23

<210> 87
<211> 29
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 87
ggtagagatg tagaaggga agcaagacc 29

<210> 88
<211> 50
<212> DNA
<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 88

gctccctacc cgtgcaggtt tcttcatttg ttcctttaac cagtatgccg 50

<210> 89

<211> 2956

<212> DNA

<213> Homo sapiens

<400> 89

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cgggatccag agcgcgcgc acttcgtcat gttcttcgcg ccctgggtgtg 300

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<210> 90
 <211> 432
 <212> PRT
 <213> Homo sapiens

<400> 90
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 Gly Gly Arg Trp Gly Ala Arg Ala Gln Glu Ala Ala Ala Ala Ala
 35 40 45
 Ala Asp Gly Pro Pro Ala Ala Asp Gly Glu Asp Gly Gln Asp Pro
 50 55 60
 His Ser Lys His Leu Tyr Thr Ala Asp Met Phe Thr His Gly Ile
 65 70 75
 Gln Ser Ala Ala His Phe Val Met Phe Phe Ala Pro Trp Cys Gly
 80 85 90
 His Cys Gln Arg Leu Gln Pro Thr Trp Asn Asp Leu Gly Asp Lys
 95 100 105
 Tyr Asn Ser Met Glu Asp Ala Lys Val Tyr Val Ala Lys Val Asp
 110 115 120
 Cys Thr Ala His Ser Asp Val Cys Ser Ala Gln Gly Val Arg Gly
 125 130 135
 Tyr Pro Thr Leu Lys Leu Phe Lys Pro Gly Gln Glu Ala Val Lys
 140 145 150
 Tyr Gln Gly Pro Arg Asp Phe Gln Thr Leu Glu Asn Trp Met Leu
 155 160 165
 Gln Thr Leu Asn Glu Glu Pro Val Thr Pro Glu Pro Glu Val Glu
 170 175 180

Pro	Pro	Ser	Ala	Pro	Glu	Leu	Lys	Gln	Gly	Leu	Tyr	Glu	Leu	Ser	185	190	195
Ala	Ser	Asn	Phe	Glu	Leu	His	Val	Ala	Gln	Gly	Asp	His	Phe	Ile	200	205	210
Lys	Phe	Phe	Ala	Pro	Trp	Cys	Gly	His	Cys	Lys	Ala	Leu	Ala	Pro	215	220	225
Thr	Trp	Glu	Gln	Leu	Ala	Leu	Gly	Leu	Glu	His	Ser	Glu	Thr	Val	230	235	240
Lys	Ile	Gly	Lys	Val	Asp	Cys	Thr	Gln	His	Tyr	Glu	Leu	Cys	Ser	245	250	255
Gly	Asn	Gln	Val	Arg	Gly	Tyr	Pro	Thr	Leu	Leu	Trp	Phe	Arg	Asp	260	265	270
Gly	Lys	Lys	Val	Asp	Gln	Tyr	Lys	Gly	Lys	Arg	Asp	Leu	Glu	Ser	275	280	285
Leu	Arg	Glu	Tyr	Val	Glu	Ser	Gln	Leu	Gln	Arg	Thr	Glu	Thr	Gly	290	295	300
Ala	Thr	Glu	Thr	Val	Thr	Pro	Ser	Glu	Ala	Pro	Val	Leu	Ala	Ala	305	310	315
Glu	Pro	Glu	Ala	Asp	Lys	Gly	Thr	Val	Leu	Ala	Leu	Thr	Glu	Asn	320	325	330
Asn	Phe	Asp	Asp	Thr	Ile	Ala	Glu	Gly	Ile	Thr	Phe	Ile	Lys	Phe	335	340	345
Tyr	Ala	Pro	Trp	Cys	Gly	His	Cys	Lys	Thr	Leu	Ala	Pro	Thr	Trp	350	355	360
Glu	Glu	Leu	Ser	Lys	Lys	Glu	Phe	Pro	Gly	Leu	Ala	Gly	Val	Lys	365	370	375
Ile	Ala	Glu	Val	Asp	Cys	Thr	Ala	Glu	Arg	Asn	Ile	Cys	Ser	Lys	380	385	390
Tyr	Ser	Val	Arg	Gly	Tyr	Pro	Thr	Leu	Leu	Leu	Phe	Arg	Gly	Gly	395	400	405
Lys	Lys	Val	Ser	Glu	His	Ser	Gly	Gly	Arg	Asp	Leu	Asp	Ser	Leu	410	415	420
His	Arg	Phe	Val	Leu	Ser	Gln	Ala	Lys	Asp	Glu	Leu				425	430	

<210> 91

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 91
atgttcttcg cgccctggtg 20

<210> 92
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 92
ccaagccaac acactctaca g 21

<210> 93
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 93
aagtggtcgc cttgtgcaac gtgc 24

<210> 94
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 94
ggtcaaaggg gatatatcgc cac 23

<210> 95
<211> 49
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 95
gcatggaaga tgccaaagtc tatgtggcta aagtggactg cacggcca 49

<210> 96
<211> 1016
<212> DNA
<213> Homo sapiens

<400> 96
cttttctgag gaaccacagc aatgaatggc tttgcatcct tgcttcgaag 50
aaaccaattt atcctcctgg tactatttct tttgcaaatt cagagtctgg 100
gtctggatat tgatagccgt cctaccgctg aagtctgtgc cacacacaca 150

atttcaccag gacccaaagg agatgatggt gaaaaaggag atccaggaga 200
agaggggaaag catggcaaag tgggacgcat ggggccgaaa ggaattaaaag 250
gagaactggg tgatatggga gatcagggca atattggcaa gactgggccc 300
attgggaaga aggggtgacaa aggggaaaaa ggtttgcttg gaatacctgg 350
agaaaaaggc aaagcaggta ctgtctgtga ttgtggaaga taccggaaat 400
ttgttggaaca actggatatt agtattgctc ggctcaagac atctatgaag 450
tttgtcaaga atgtgatagc agggattagg gaaactgaag agaaattcta 500
ctacatcgtg caggaagaga agaactacag ggaatcccta acccactgca 550
ggattcgggg tggaatgcta gccatgccc aggatgaagc tgccaacaca 600
ctcatcgctg actatgttgc caagagtggc ttctttcggg tgttcattgg 650
cgtgaatgac cttgaaaggg agggacagta catgtccaca gacaacactc 700
cactgcagaa ctatagcaac tggaatgagg gggaaccag cgaccctat 750
ggatcatgagg actgtgtgga gatgctgagc tctggcagat ggaatgacac 800
agagtgccat cttaccatgt actttgtctg tgagttcatc aagaagaaaa 850
agtaacttcc ctcacacctac gtatttgcta ttttctgtg accgtcatta 900
cagttattgt tatccatcct ttttttctg attgtactac atttgatctg 950
agtcaacata gctagaaaaat gctaaaactga ggtatggagc ctccatcatc 1000
aaaaaaaaaa aaaaaa 1016

<210> 97
<211> 277
<212> PRT
<213> Homo sapiens

<400> 97
Met Asn Gly Phe Ala Ser Leu Leu Arg Arg Asn Gln Phe Ile Leu
1 5 10 15
Leu Val Leu Phe Leu Leu Gln Ile Gln Ser Leu Gly Leu Asp Ile
20 25 30
Asp Ser Arg Pro Thr Ala Glu Val Cys Ala Thr His Thr Ile Ser
35 40 45
Pro Gly Pro Lys Gly Asp Asp Gly Glu Lys Gly Asp Pro Gly Glu
50 55 60
Glu Gly Lys His Gly Lys Val Gly Arg Met Gly Pro Lys Gly Ile
65 70 75
Lys Gly Glu Leu Gly Asp Met Gly Asp Gln Gly Asn Ile Gly Lys

	80		85		90
Thr Gly Pro Ile	Gly Lys Lys Gly Asp	Lys Gly Glu Lys Gly	Leu		
	95	100	105		
Leu Gly Ile Pro	Gly Glu Lys Gly Lys	Ala Gly Thr Val Cys	Asp		
	110	115	120		
Cys Gly Arg Tyr	Arg Lys Phe Val Gly	Gln Leu Asp Ile Ser	Ile		
	125	130	135		
Ala Arg Leu Lys	Thr Ser Met Lys Phe	Val Lys Asn Val Ile	Ala		
	140	145	150		
Gly Ile Arg Glu	Thr Glu Glu Lys Phe	Tyr Tyr Ile Val Gln	Glu		
	155	160	165		
Glu Lys Asn Tyr	Arg Glu Ser Leu Thr	His Cys Arg Ile Arg	Gly		
	170	175	180		
Gly Met Leu Ala	Met Pro Lys Asp Glu	Ala Ala Asn Thr Leu	Ile		
	185	190	195		
Ala Asp Tyr Val	Ala Lys Ser Gly Phe	Phe Arg Val Phe Ile	Gly		
	200	205	210		
Val Asn Asp Leu	Glu Arg Glu Gly Gln	Tyr Met Ser Thr Asp	Asn		
	215	220	225		
Thr Pro Leu Gln	Asn Tyr Ser Asn Trp	Asn Glu Gly Glu Pro	Ser		
	230	235	240		
Asp Pro Tyr Gly	His Glu Asp Cys Val	Glu Met Leu Ser Ser	Gly		
	245	250	255		
Arg Trp Asn Asp	Thr Glu Cys His Leu	Thr Met Tyr Phe Val	Cys		
	260	265	270		
Glu Phe Ile Lys	Lys Lys Lys				
	275				

<210> 98

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 98

cgctgactat gttgccaaga gtgg 24

<210> 99

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 99

gatgatggag gctccatacc tcag 24

<210> 100

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 100

gtgttcattg gcgatgaatga ccttgaaagg gagggacagt acatgttcac 50

<210> 101

<211> 2574

<212> DNA

<213> Homo sapiens

<400> 101

ggtttctatcg attcgaattc ggccacactg gccggatcct ctagagatcc 50

ctogacctcg acccacgcgt ccgctgctct ccgcccgtgt ggagtgggtgg 100

gggcctgggt gggaatgggc gtgtgccagc gcacgcgcgc tccctggaag 150

gagaagtctc agctagaacg agcggcccta ggttttcgga agggaggatc 200

agggatgttt gcgagcggct ggaaccagac ggtgccgata gaggaagcgg 250

gctccatggc tgcctcctcg ctgctgcccc tgctgctgtt gctaccgctg 300

ctgctgctga agctacacct ctggccgcag ttgcgctggc ttccggcgga 350

cttggccttt gcggtgcgag ctctgtgctg caaaagggtt cttcgagctc 400

gcgccctggc cgcggctgcc gccgaccgg aaggtcccga ggggggctgc 450

agcctggcct ggcgccctgc ggaactggcc cagcagcgcg ccgcgcacac 500

ctttctcatt cacggctcgc ggcgttttag ctactcagag gcggagcgcg 550

agagtaacag ggctgcacgc gccttcctac gtgcgctagg ctgggactgg 600

ggacccgacg gcggcgacag cggcgagggg agcgtggag aaggcgagcg 650

ggcagcgccg ggagccggag atgcagcggc cggaagcggc gcggagtgtg 700

ccggaggggg cgggtgccgc agaggtggag gagccgccgc ccctctgtca 750

cctggagcaa ctgtggcgct gtcctcccc gctggcccag agtttctgtg 800

gctctggttc gggtggcca aggcggcct gcgcactgcc tttgtgcca 850

ccgccctgcg ccggggcccc ctgctgcact gcctccgcag ctgcggcgcg 900

cgcgcgctgg tgctggcgcc agagtttctg gagtccctgg agccggacct 950
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 ggtgtccacc aggaagatgt gatctacctc gccctccac tctaccacat 1250
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 tgggtgctgaa atccaagttc tcggctggtc agttctggga agattgccag 1350
 cagcacaggg tgacggtgtt ccagtacatt ggggagctgt gccgatacct 1400
 tgtcaaccag ccccgagca aggcagaacg tggccataag gtccggctgg 1450
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 gtcttcgggc ctggggatgt tttcttcaac actggggacc tgctgggtctg 1850
 cgatgaccaa ggttttctcc gcttccatga tcgtactgga gacaccttca 1900
 ggtggaaggg ggagaatgtg gccacaaccg aggtggcaga ggtcttcgag 1950
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 ctttggaacct tatgcagctc tacaccacg tgtctgagaa cttgccacct 2100
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 gaccttcaaa cagcagaaag ttcggatggc aaatgagggc ttcgaccca 2200
 gcacctgtc tgaccactg tacgttctgg accaggctgt aggtgcctac 2250
 ctgccccca caactgccc gtacagcgc ctctggcag gaaaccttcg 2300
 aatctgagaa cttccacacc tgaggcacct gagagaggaa ctctgtgggg 2350

tggggggccgt tgcagggtgta ctgggctgtc agggatcttt tctataccag 2400
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 actctagagt cgacctgcag tagggataac agggtaataa gcttggccgc 2550
 catggcccaa cttgtttatt gcag 2574

<210> 102
 <211> 730
 <212> PRT
 <213> Homo sapiens

<400> 102
 Met Gly Val Cys Gln Arg Thr Arg Ala Pro Trp Lys Glu Lys Ser
 1 5 10 15
 Gln Leu Glu Arg Ala Ala Leu Gly Phe Arg Lys Gly Gly Ser Gly
 20 25 30
 Met Phe Ala Ser Gly Trp Asn Gln Thr Val Pro Ile Glu Glu Ala
 35 40 45
 Gly Ser Met Ala Ala Leu Leu Leu Leu Pro Leu Leu Leu Leu Leu
 50 55 60
 Pro Leu Leu Leu Leu Lys Leu His Leu Trp Pro Gln Leu Arg Trp
 65 70 75
 Leu Pro Ala Asp Leu Ala Phe Ala Val Arg Ala Leu Cys Cys Lys
 80 85 90
 Arg Ala Leu Arg Ala Arg Ala Leu Ala Ala Ala Ala Asp Pro
 95 100 105
 Glu Gly Pro Glu Gly Gly Cys Ser Leu Ala Trp Arg Leu Ala Glu
 110 115 120
 Leu Ala Gln Gln Arg Ala Ala His Thr Phe Leu Ile His Gly Ser
 125 130 135
 Arg Arg Phe Ser Tyr Ser Glu Ala Glu Arg Glu Ser Asn Arg Ala
 140 145 150
 Ala Arg Ala Phe Leu Arg Ala Leu Gly Trp Asp Trp Gly Pro Asp
 155 160 165
 Gly Gly Asp Ser Gly Glu Gly Ser Ala Gly Glu Gly Glu Arg Ala
 170 175 180
 Ala Pro Gly Ala Gly Asp Ala Ala Ala Gly Ser Gly Ala Glu Phe
 185 190 195
 Ala Gly Gly Asp Gly Ala Ala Arg Gly Gly Gly Ala Ala Ala Pro
 200 205 210

Leu	Ser	Pro	Gly	Ala	Thr	Val	Ala	Leu	Leu	Leu	Pro	Ala	Gly	Pro	215	220	225
Glu	Phe	Leu	Trp	Leu	Trp	Phe	Gly	Leu	Ala	Lys	Ala	Gly	Leu	Arg	230	235	240
Thr	Ala	Phe	Val	Pro	Thr	Ala	Leu	Arg	Arg	Gly	Pro	Leu	Leu	His	245	250	255
Cys	Leu	Arg	Ser	Cys	Gly	Ala	Arg	Ala	Leu	Val	Leu	Ala	Pro	Glu	260	265	270
Phe	Leu	Glu	Ser	Leu	Glu	Pro	Asp	Leu	Pro	Ala	Leu	Arg	Ala	Met	275	280	285
Gly	Leu	His	Leu	Trp	Ala	Ala	Gly	Pro	Gly	Thr	His	Pro	Ala	Gly	290	295	300
Ile	Ser	Asp	Leu	Leu	Ala	Glu	Val	Ser	Ala	Glu	Val	Asp	Gly	Pro	305	310	315
Val	Pro	Gly	Tyr	Leu	Ser	Ser	Pro	Gln	Ser	Ile	Thr	Asp	Thr	Cys	320	325	330
Leu	Tyr	Ile	Phe	Thr	Ser	Gly	Thr	Thr	Gly	Leu	Pro	Lys	Ala	Ala	335	340	345
Arg	Ile	Ser	His	Leu	Lys	Ile	Leu	Gln	Cys	Gln	Gly	Phe	Tyr	Gln	350	355	360
Leu	Cys	Gly	Val	His	Gln	Glu	Asp	Val	Ile	Tyr	Leu	Ala	Leu	Pro	365	370	375
Leu	Tyr	His	Met	Ser	Gly	Ser	Leu	Leu	Gly	Ile	Val	Gly	Cys	Met	380	385	390
Gly	Ile	Gly	Ala	Thr	Val	Val	Leu	Lys	Ser	Lys	Phe	Ser	Ala	Gly	395	400	405
Gln	Phe	Trp	Glu	Asp	Cys	Gln	Gln	His	Arg	Val	Thr	Val	Phe	Gln	410	415	420
Tyr	Ile	Gly	Glu	Leu	Cys	Arg	Tyr	Leu	Val	Asn	Gln	Pro	Pro	Ser	425	430	435
Lys	Ala	Glu	Arg	Gly	His	Lys	Val	Arg	Leu	Ala	Val	Gly	Ser	Gly	440	445	450
Leu	Arg	Pro	Asp	Thr	Trp	Glu	Arg	Phe	Val	Arg	Arg	Phe	Gly	Pro	455	460	465
Leu	Gln	Val	Leu	Glu	Thr	Tyr	Gly	Leu	Thr	Glu	Gly	Asn	Val	Ala	470	475	480
Thr	Ile	Asn	Tyr	Thr	Gly	Gln	Arg	Gly	Ala	Val	Gly	Arg	Ala	Ser	485	490	495
Trp	Leu	Tyr	Lys	His	Ile	Phe	Pro	Phe	Ser	Leu	Ile	Arg	Tyr	Asp			

					500						505						510
Val	Thr	Thr	Gly	Glu	Pro	Ile	Arg	Asp	Pro	Gln	Gly	His	Cys	Met	515	520	525
Ala	Thr	Ser	Pro	Gly	Glu	Pro	Gly	Leu	Leu	Val	Ala	Pro	Val	Ser	530	535	540
Gln	Gln	Ser	Pro	Phe	Leu	Gly	Tyr	Ala	Gly	Gly	Pro	Glu	Leu	Ala	545	550	555
Gln	Gly	Lys	Leu	Leu	Lys	Asp	Val	Phe	Arg	Pro	Gly	Asp	Val	Phe	560	565	570
Phe	Asn	Thr	Gly	Asp	Leu	Leu	Val	Cys	Asp	Asp	Gln	Gly	Phe	Leu	575	580	585
Arg	Phe	His	Asp	Arg	Thr	Gly	Asp	Thr	Phe	Arg	Trp	Lys	Gly	Glu	590	595	600
Asn	Val	Ala	Thr	Thr	Glu	Val	Ala	Glu	Val	Phe	Glu	Ala	Leu	Asp	605	610	615
Phe	Leu	Gln	Glu	Val	Asn	Val	Tyr	Gly	Val	Thr	Val	Pro	Gly	His	620	625	630
Glu	Gly	Arg	Ala	Gly	Met	Ala	Ala	Leu	Val	Leu	Arg	Pro	Pro	His	635	640	645
Ala	Leu	Asp	Leu	Met	Gln	Leu	Tyr	Thr	His	Val	Ser	Glu	Asn	Leu	650	655	660
Pro	Pro	Tyr	Ala	Arg	Pro	Arg	Phe	Leu	Arg	Leu	Gln	Glu	Ser	Leu	665	670	675
Ala	Thr	Thr	Glu	Thr	Phe	Lys	Gln	Gln	Lys	Val	Arg	Met	Ala	Asn	680	685	690
Glu	Gly	Phe	Asp	Pro	Ser	Thr	Leu	Ser	Asp	Pro	Leu	Tyr	Val	Leu	695	700	705
Asp	Gln	Ala	Val	Gly	Ala	Tyr	Leu	Pro	Leu	Thr	Thr	Ala	Arg	Tyr	710	715	720
Ser	Ala	Leu	Leu	Ala	Gly	Asn	Leu	Arg	Ile						725	730	

<210> 103

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 103

gagagccatg gggctccacc tg 22

<210> 104
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 104
ggagaatgtg gccacaac 18

<210> 105
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 105
gccctggcac agtgactcca tagacg 26

<210> 106
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 106
atccacttca gcggacac 18

<210> 107
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 107
ccagtgccag gatacctctc ttccccccag agcataacag acacg 45

<210> 108
<211> 2579
<212> DNA
<213> Homo sapiens

<400> 108
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cctccacgca cacacatccc caagaacctc gagctcacac caacagacac 100
acgcgcgcat acacactcgc tctcgtttgt ccatctccct cccgggggag 150
ccggcgcgcg ctccacctt tgccgcacac tccggcgagc cgagcccgcg 200

gcgctccagg attctgcggc tcggaactcg gattgcagct ctgaaccccc 250
atggtggttt tttaaacact tcttttcott ctcttctctg ttttgattgc 300
accgtttcca tctgggggct agaggagcaa ggcagcagcc ttcccagcca 350
gcccttggtg gcttgccatc gtccatctgg cttataaaag tttgctgagc 400
gcagtccaga gggctgcgct gctcgtcccc tcggctggca gaaggggggtg 450
acgctgggca gcggcgagga gcgcgccgct gcctctggcg ggctttcggc 500
ttgaggggca aggtgaagag cgcaccggcc gtgggggtta ccgagctgga 550
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cttggggctg ctgctctccc tccccgccg ggcggatgtg aaggctcgga 650
gctgcggaga ggtccgccag gcgtacgggtg ccaagggatt cagcctggcg 700
gacatcccc accaggagat cgcaggggaa cacttaagaa tctgtctca 750
ggaatataca tgctgcacca cagaaatgga agacaagta agccaacaaa 800
gcaaactcga atttgaaaac cttgtggaag agacaagcca ttttgctgcg 850
accacttttg tgtccaggca taagaaatct gacgaatttt tccgagagct 900
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cagctcaagc catttgagga cgtgccccgg aaactgaaga ttcagggtac 1200
ccgcgccttc attgctgcca ggacctttgt ccaggggctg actgtgggca 1250
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cctgctccag ccctcagatc tgcccgtca gctcctgaaa attttaatac 1650

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 aaaaaggtct ggtcagcatt accctacact atctgcaagg acgagagcgt 1800
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 gcagattatg gctctccgtg tgatgaccaa caaactaaaa aacgcctaca 2000
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 gggagtggca gtgggtgcat ggatgacgtg tgtcccacgg agtttgagtt 2100
 tgtcaccaca gaggcccccg cagtggatcc cgaccggaga gaggtggact 2150
 cttctgcagc ccagcgtggc cactccctgc tctcctggtc tctcacctgc 2200
 attgtcctgg cactgcagag actgtgcaga taatcttggg tttttggtca 2250
 gatgaaactg catttttagct atctgaatgg ccaactcact tcttttctta 2300
 cactcttggg caatggacca tgccacaaaa acttaccgtt ttctatgaga 2350
 agagagcagt aatgcaatct gcctcccttt ttgttttccc aaagagtacc 2400
 gggtgccaga ctgaactgct tctcttttcc ttcagctatc tgtggggacc 2450
 ttgtttattc tagagagaat tcttactcaa atttttcgta ccaggagatt 2500
 ttcttacctt catttgcttt tatgctgcag aagtaaagga atctcacgtt 2550
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<210> 109
 <211> 555
 <212> PRT
 <213> Homo sapiens

<400> 109
 Met Pro Ser Trp Ile Gly Ala Val Ile Leu Pro Leu Leu Gly Leu
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 Leu Leu Ser Leu Pro Ala Gly Ala Asp Val Lys Ala Arg Ser Cys
 20 25 30
 Gly Glu Val Arg Gln Ala Tyr Gly Ala Lys Gly Phe Ser Leu Ala
 35 40 45
 Asp Ile Pro Tyr Gln Glu Ile Ala Gly Glu His Leu Arg Ile Cys
 50 55 60
 Pro Gln Glu Tyr Thr Cys Cys Thr Thr Glu Met Glu Asp Lys Leu
 65 70 75

Ser	Gln	Gln	Ser	Lys	Leu	Glu	Phe	Glu	Asn	Leu	Val	Glu	Glu	Thr	
				80					85					90	
Ser	His	Phe	Val	Arg	Thr	Thr	Phe	Val	Ser	Arg	His	Lys	Lys	Phe	
				95					100					105	
Asp	Glu	Phe	Phe	Arg	Glu	Leu	Leu	Glu	Asn	Ala	Glu	Lys	Ser	Leu	
				110					115					120	
Asn	Asp	Met	Phe	Val	Arg	Thr	Tyr	Gly	Met	Leu	Tyr	Met	Gln	Asn	
				125					130					135	
Ser	Glu	Val	Phe	Gln	Asp	Leu	Phe	Thr	Glu	Leu	Lys	Arg	Tyr	Tyr	
				140					145					150	
Thr	Gly	Gly	Asn	Val	Asn	Leu	Glu	Glu	Met	Leu	Asn	Asp	Phe	Trp	
				155					160					165	
Ala	Arg	Leu	Leu	Glu	Arg	Met	Phe	Gln	Leu	Ile	Asn	Pro	Gln	Tyr	
				170					175					180	
His	Phe	Ser	Glu	Asp	Tyr	Leu	Glu	Cys	Val	Ser	Lys	Tyr	Thr	Asp	
				185					190					195	
Gln	Leu	Lys	Pro	Phe	Gly	Asp	Val	Pro	Arg	Lys	Leu	Lys	Ile	Gln	
				200					205					210	
Val	Thr	Arg	Ala	Phe	Ile	Ala	Ala	Arg	Thr	Phe	Val	Gln	Gly	Leu	
				215					220					225	
Thr	Val	Gly	Arg	Glu	Val	Ala	Asn	Arg	Val	Ser	Lys	Val	Ser	Pro	
				230					235					240	
Thr	Pro	Gly	Cys	Ile	Arg	Ala	Leu	Met	Lys	Met	Leu	Tyr	Cys	Pro	
				245					250					255	
Tyr	Cys	Arg	Gly	Leu	Pro	Thr	Val	Arg	Pro	Cys	Asn	Asn	Tyr	Cys	
				260					265					270	
Leu	Asn	Val	Met	Lys	Gly	Cys	Leu	Ala	Asn	Gln	Ala	Asp	Leu	Asp	
				275					280					285	
Thr	Glu	Trp	Asn	Leu	Phe	Ile	Asp	Ala	Met	Leu	Leu	Val	Ala	Glu	
				290					295					300	
Arg	Leu	Glu	Gly	Pro	Phe	Asn	Ile	Glu	Ser	Val	Met	Asp	Pro	Ile	
				305					310					315	
Asp	Val	Lys	Ile	Ser	Glu	Ala	Ile	Met	Asn	Met	Gln	Glu	Asn	Ser	
				320					325					330	
Met	Gln	Val	Ser	Ala	Lys	Val	Phe	Gln	Gly	Cys	Gly	Gln	Pro	Lys	
				335					340					345	
Pro	Ala	Pro	Ala	Leu	Arg	Ser	Ala	Arg	Ser	Ala	Pro	Glu	Asn	Phe	
				350					355					360	
Asn	Thr	Arg	Phe	Arg	Pro	Tyr	Asn	Pro	Glu	Glu	Arg	Pro	Thr	Thr	

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380	385	390
Lys Leu Lys Leu Ser Lys Lys Val Trp Ser Ala Leu Pro Tyr Thr		
395	400	405
Ile Cys Lys Asp Glu Ser Val Thr Ala Gly Thr Ser Asn Glu Glu		
410	415	420
Glu Cys Trp Asn Gly His Ser Lys Ala Arg Tyr Leu Pro Glu Ile		
425	430	435
Met Asn Asp Gly Leu Thr Asn Gln Ile Asn Asn Pro Glu Val Asp		
440	445	450
Val Asp Ile Thr Arg Pro Asp Thr Phe Ile Arg Gln Gln Ile Met		
455	460	465
Ala Leu Arg Val Met Thr Asn Lys Leu Lys Asn Ala Tyr Asn Gly		
470	475	480
Asn Asp Val Asn Phe Gln Asp Thr Ser Asp Glu Ser Ser Gly Ser		
485	490	495
Gly Ser Gly Ser Gly Cys Met Asp Asp Val Cys Pro Thr Glu Phe		
500	505	510
Glu Phe Val Thr Thr Glu Ala Pro Ala Val Asp Pro Asp Arg Arg		
515	520	525
Glu Val Asp Ser Ser Ala Ala Gln Arg Gly His Ser Leu Leu Ser		
530	535	540
Trp Ser Leu Thr Cys Ile Val Leu Ala Leu Gln Arg Leu Cys Arg		
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<220>
 <223> Synthetic oligonucleotide probe

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<210> 111
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 <212> DNA
 <213> Artificial Sequence

<220>
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<400> 111

tgcacagtct ctgcagtgcc cagg 24

<210> 112

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<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 112

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<210> 113

<211> 4649

<212> DNA

<213> Homo sapiens

<400> 113

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<210> 114

<211> 515

<212> PRT

<213> Homo sapiens

<400> 114

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				20					25					30
Ala	Gly	Phe	Trp	Ile	Leu	Cys	Leu	Leu	Thr	Tyr	Gly	Tyr	Leu	Ser
				35					40					45
Trp	Gly	Gln	Ala	Leu	Glu	Glu	Glu	Glu	Glu	Gly	Ala	Leu	Leu	Ala
				50					55					60
Gln	Ala	Gly	Glu	Lys	Leu	Glu	Pro	Ser	Thr	Thr	Ser	Thr	Ser	Gln
				65					70					75
Pro	His	Leu	Ile	Phe	Ile	Leu	Ala	Asp	Asp	Gln	Gly	Phe	Arg	Asp
				80					85					90
Val	Gly	Tyr	His	Gly	Ser	Glu	Ile	Lys	Thr	Pro	Thr	Leu	Asp	Lys
				95					100					105
Leu	Ala	Ala	Glu	Gly	Val	Lys	Leu	Glu	Asn	Tyr	Tyr	Val	Gln	Pro

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125	130	135
Ile His Thr Gly Leu Gln His Ser Ile	Ile Arg Pro Thr Gln Pro	
140	145	150
Asn Cys Leu Pro Leu Asp Asn Ala Thr	Leu Pro Gln Lys Leu Lys	
155	160	165
Glu Val Gly Tyr Ser Thr His Met Val	Gly Lys Trp His Leu Gly	
170	175	180
Phe Asn Arg Lys Glu Cys Met Pro Thr	Arg Arg Gly Phe Asp Thr	
185	190	195
Phe Phe Gly Ser Leu Leu Gly Ser Gly	Asp Tyr Tyr Thr His Tyr	
200	205	210
Lys Cys Asp Ser Pro Gly Met Cys Gly	Tyr Asp Leu Tyr Glu Asn	
215	220	225
Asp Asn Ala Ala Trp Asp Tyr Asp Asn	Gly Ile Tyr Ser Thr Gln	
230	235	240
Met Tyr Thr Gln Arg Val Gln Gln Ile	Leu Ala Ser His Asn Pro	
245	250	255
Thr Lys Pro Ile Phe Leu Tyr Thr Ala	Tyr Gln Ala Val His Ser	
260	265	270
Pro Leu Gln Ala Pro Gly Arg Tyr Phe	Glu His Tyr Arg Ser Ile	
275	280	285
Ile Asn Ile Asn Arg Arg Arg Tyr Ala	Ala Met Leu Ser Cys Leu	
290	295	300
Asp Glu Ala Ile Asn Asn Val Thr Leu	Ala Leu Lys Thr Tyr Gly	
305	310	315
Phe Tyr Asn Asn Ser Ile Ile Ile Tyr	Ser Ser Asp Asn Gly Gly	
320	325	330
Gln Pro Thr Ala Gly Gly Ser Asn Trp	Pro Leu Arg Gly Ser Lys	
335	340	345
Gly Thr Tyr Trp Glu Gly Gly Ile Arg	Ala Val Gly Phe Val His	
350	355	360
Ser Pro Leu Leu Lys Asn Lys Gly Thr	Val Cys Lys Glu Leu Val	
365	370	375
His Ile Thr Asp Trp Tyr Pro Thr Leu	Ile Ser Leu Ala Glu Gly	
380	385	390
Gln Ile Asp Glu Asp Ile Gln Leu Asp	Gly Tyr Asp Ile Trp Glu	
395	400	405

Thr	Ile	Ser	Glu	Gly	Leu	Arg	Ser	Pro	Arg	Val	Asp	Ile	Leu	His
				410					415					420
Asn	Ile	Asp	Pro	Tyr	Thr	Pro	Arg	Gln	Lys	Met	Ala	Pro	Gly	Gln
				425					430					435
Gln	Ala	Met	Gly	Ser	Gly	Thr	Leu	Gln	Ser	Ser	Gln	Pro	Ser	Glu
				440					445					450
Cys	Ser	Thr	Gly	Asn	Cys	Leu	Gln	Glu	Ile	Leu	Ala	Thr	Ala	Thr
				455					460					465
Gly	Ser	Pro	Leu	Ser	Leu	Ser	Ala	Thr	Trp	Asp	Arg	Thr	Gly	Gly
				470					475					480
Thr	Met	Asn	Gly	Ser	Pro	Cys	Gln	Leu	Ala	Lys	Val	Tyr	Gly	Phe
				485					490					495
Ser	Thr	Ser	Gln	Pro	Thr	His	Met	Arg	Gly	Trp	Thr	Tyr	Leu	Thr
				500					505					510
Gly	Ile	Gln	Glu	Ser										
				515										

- <210> 115
- <211> 24
- <212> DNA
- <213> Artificial Sequence
- <220>
- <223> Synthetic oligonucleotide probe
- <400> 115
- cccaacccaa ctgtttacct ctgg 24
- <210> 116
- <211> 24
- <212> DNA
- <213> Artificial Sequence
- <220>
- <223> Synthetic oligonucleotide probe
- <400> 116
- ctctctgagt gtacatctgt gtgg 24
- <210> 117
- <211> 53
- <212> DNA
- <213> Artificial Sequence
- <220>
- <223> Synthetic oligonucleotide probe
- <220>
- <221> unsure
- <222> 33
- <223> unknown base

<400> 117
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cgg 53
<210> 118
<211> 2260
<212> DNA
<213> Homo sapiens
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<221> unsure
<222> 2009, 2026, 2033, 2055, 2074, 2078, 2086
<223> unknown base
<400> 118
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gtaataataa 2260

<210> 119
<211> 338
<212> PRT
<213> Homo sapiens

<400> 119
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Leu	Leu	Ala	Ser	Ala	Arg	Gln	Pro	Gly	Val	Cys	His	Tyr	Gly	Thr	
				35					40					45	
Lys	Leu	Ala	Cys	Cys	Tyr	Gly	Trp	Arg	Arg	Asn	Ser	Lys	Gly	Val	
				50					55					60	
Cys	Glu	Ala	Thr	Cys	Glu	Pro	Gly	Cys	Lys	Phe	Gly	Glu	Cys	Val	
				65					70					75	
Gly	Pro	Asn	Lys	Cys	Arg	Cys	Phe	Pro	Gly	Tyr	Thr	Gly	Lys	Thr	
				80					85					90	
Cys	Ser	Gln	Asp	Val	Asn	Glu	Cys	Gly	Met	Lys	Pro	Arg	Pro	Cys	
				95					100					105	
Gln	His	Arg	Cys	Val	Asn	Thr	His	Gly	Ser	Tyr	Lys	Cys	Phe	Cys	
				110					115					120	
Leu	Ser	Gly	His	Met	Leu	Met	Pro	Asp	Ala	Thr	Cys	Val	Asn	Ser	
				125					130					135	
Arg	Thr	Cys	Ala	Met	Ile	Asn	Cys	Gln	Tyr	Ser	Cys	Glu	Asp	Thr	
				140					145					150	
Glu	Glu	Gly	Pro	Gln	Cys	Leu	Cys	Pro	Ser	Ser	Gly	Leu	Arg	Leu	
				155					160					165	
Ala	Pro	Asn	Gly	Arg	Asp	Cys	Leu	Asp	Ile	Asp	Glu	Cys	Ala	Ser	
				170					175					180	
Gly	Lys	Val	Ile	Cys	Pro	Tyr	Asn	Arg	Arg	Cys	Val	Asn	Thr	Phe	
				185					190					195	
Gly	Ser	Tyr	Tyr	Cys	Lys	Cys	His	Ile	Gly	Phe	Glu	Leu	Gln	Tyr	
				200					205					210	
Ile	Ser	Gly	Arg	Tyr	Asp	Cys	Ile	Asp	Ile	Asn	Glu	Cys	Thr	Met	
				215					220					225	
Asp	Ser	His	Thr	Cys	Ser	His	His	Ala	Asn	Cys	Phe	Asn	Thr	Gln	
				230					235					240	
Gly	Ser	Phe	Lys	Cys	Lys	Cys	Lys	Gln	Gly	Tyr	Lys	Gly	Asn	Gly	
				245					250					255	
Leu	Arg	Cys	Ser	Ala	Ile	Pro	Glu	Asn	Ser	Val	Lys	Glu	Val	Leu	
				260					265					270	
Arg	Ala	Pro	Gly	Thr	Ile	Lys	Asp	Arg	Ile	Lys	Lys	Leu	Leu	Ala	
				275					280					285	
His	Lys	Asn	Ser	Met	Lys	Lys	Lys	Ala	Lys	Ile	Lys	Asn	Val	Thr	
				290					295					300	
Pro	Glu	Pro	Thr	Arg	Thr	Pro	Thr	Pro	Lys	Val	Asn	Leu	Gln	Pro	

	305		310		315									
Phe	Asn	Tyr	Glu	Glu	Ile	Val	Ser	Arg	Gly	Gly	Asn	Ser	His	Gly
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Gly	Lys	Lys	Gly	Asn	Glu	Glu	Lys							
	335													

<210> 120
 <211> 22
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 120
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<210> 121
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 121
 ggctgcacgt atggctatcc atag 24

<210> 122
 <211> 50
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 122
 gataaactgt cagtacagct gtgaagacac agaagaagg ccacagtgcc 50

<210> 123
 <211> 1199
 <212> DNA
 <213> Homo sapiens

<400> 123
 gggagctgct gctgtggctg ctggtgctgt gcgcgtgct cctgctcttg 50
 gtgcagctgc tgcgcttcct gagggctgac ggcgacctga cgtactatg 100
 ggccagagtgg cagggacgac gcccagaatg ggagctgact gatatggtgg 150
 tgtgggtgac tggagcctcg agtgaattg gtgaggagct ggcttaccag 200
 ttgtctaaac taggagtttc tcttgctgctg tcagccagaa gagtgcata 250
 gctggaaagg gtgaaaagaa gatgcctaga gaatggcaat ttaaaagaaa 300

80										85					90				
Met	Ser	Gln	Arg	Ser	Leu	Cys	Met	Asp	Thr	Ser	Leu	Asp	Val	Tyr					
				95					100					105					
Arg	Lys	Leu	Ile	Glu	Leu	Asn	Tyr	Leu	Gly	Thr	Val	Ser	Leu	Thr					
				110					115					120					
Lys	Cys	Val	Leu	Pro	His	Met	Ile	Glu	Arg	Lys	Gln	Gly	Lys	Ile					
				125					130					135					
Val	Thr	Val	Asn	Ser	Ile	Leu	Gly	Ile	Ile	Ser	Val	Pro	Leu	Ser					
				140					145					150					
Ile	Gly	Tyr	Cys	Ala	Ser	Lys	His	Ala	Leu	Arg	Gly	Phe	Phe	Asn					
				155					160					165					
Gly	Leu	Arg	Thr	Glu	Leu	Ala	Thr	Tyr	Pro	Gly	Ile	Ile	Val	Ser					
				170					175					180					
Asn	Ile	Cys	Pro	Gly	Pro	Val	Gln	Ser	Asn	Ile	Val	Glu	Asn	Ser					
				185					190					195					
Leu	Ala	Gly	Glu	Val	Thr	Lys	Thr	Ile	Gly	Asn	Asn	Gly	Asp	Gln					
				200					205					210					
Ser	His	Lys	Met	Thr	Thr	Ser	Arg	Cys	Val	Arg	Leu	Met	Leu	Ile					
				215					220					225					
Ser	Met	Ala	Asn	Asp	Leu	Lys	Glu	Val	Trp	Ile	Ser	Glu	Gln	Pro					
				230					235					240					
Phe	Leu	Leu	Val	Thr	Tyr	Leu	Trp	Gln	Tyr	Met	Pro	Thr	Trp	Ala					
				245					250					255					
Trp	Trp	Ile	Thr	Asn	Lys	Met	Gly	Lys	Lys	Arg	Ile	Glu	Asn	Phe					
				260					265					270					
Lys	Ser	Gly	Val	Asp	Ala	Asp	Ser	Ser	Tyr	Phe	Lys	Ile	Phe	Lys					
				275					280					285					

Thr Lys His Asp

<210> 125
 <211> 19
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 125
 gcaatgaact gggagctgc 19

<210> 126
 <211> 19
 <212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 126

ctgtgaatag catcctggg 19

<210> 127

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 127

cttttcaagc cactggaggg 20

<210> 128

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 128

ctgtagacat ccaagctggt atcc 24

<210> 129

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 129

aagagtctgc atccacacca ctc 23

<210> 130

<211> 46

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 130

acctgacgct actatggggc gagtggcagg gacgacgccc agaagtg 46

<210> 131

<211> 2365

<212> DNA

<213> Homo sapiens

<400> 131

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caatcaatcc aacagcatat tcggttgcat cttctacaca ctacagctat 150
tgtaggttg cctgoggaca cgctgggcct ctgtcctgat gctgctgagc 200
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aatggagcgt agggctgggg accagaccgg aggagtgggg cctgaagcag 1450

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Leu	Thr	Ala	Ala	His	Cys	Phe	Glu	Lys	Ala	Ala	Ala	Thr	Glu	Leu	
				95					100					105	
Asn	Ser	Trp	Ser	Val	Val	Leu	Gly	Ser	Leu	Gln	Arg	Glu	Gly	Leu	
				110					115					120	
Ser	Pro	Gly	Ala	Glu	Glu	Val	Gly	Val	Ala	Ala	Leu	Gln	Leu	Pro	
				125					130					135	
Arg	Ala	Tyr	Asn	His	Tyr	Ser	Gln	Gly	Ser	Asp	Leu	Ala	Leu	Leu	
				140					145					150	
Gln	Leu	Ala	His	Pro	Thr	Thr	His	Thr	Pro	Leu	Cys	Leu	Pro	Gln	
				155					160					165	
Pro	Ala	His	Arg	Phe	Pro	Phe	Gly	Ala	Ser	Cys	Trp	Ala	Thr	Gly	
				170					175					180	
Trp	Asp	Gln	Asp	Thr	Ser	Asp	Ala	Pro	Gly	Thr	Leu	Arg	Asn	Leu	
				185					190					195	
Arg	Leu	Arg	Leu	Ile	Ser	Arg	Pro	Thr	Cys	Asn	Cys	Ile	Tyr	Asn	
				200					205					210	
Gln	Leu	His	Gln	Arg	His	Leu	Ser	Asn	Pro	Ala	Arg	Pro	Gly	Met	
				215					220					225	
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				230					235					240	
Asp	Ser	Gly	Gly	Pro	Val	Leu	Cys	Leu	Glu	Pro	Asp	Gly	His	Trp	
				245					250					255	
Val	Gln	Ala	Gly	Ile	Ile	Ser	Phe	Ala	Ser	Ser	Cys	Ala	Gln	Glu	
				260					265					270	
Asp	Ala	Pro	Val	Leu	Leu	Thr	Asn	Thr	Ala	Ala	His	Ser	Ser	Trp	
				275					280					285	
Leu	Gln	Ala	Arg	Val	Gln	Gly	Ala	Ala	Phe	Leu	Ala	Gln	Ser	Pro	
				290					295					300	
Glu	Thr	Pro	Glu	Met	Ser	Asp	Glu	Asp	Ser	Cys	Val	Ala	Cys	Gly	
				305					310					315	
Ser	Leu	Arg	Thr	Ala	Gly	Pro	Gln	Ala	Gly	Ala	Pro	Ser	Pro	Trp	
				320					325					330	
Pro	Trp	Glu	Ala	Arg	Leu	Met	His	Gln	Gly	Gln	Leu	Ala	Cys	Gly	
				335					340					345	
Gly	Ala	Leu	Val	Ser	Glu	Glu	Ala	Val	Leu	Thr	Ala	Ala	His	Cys	
				350					355					360	
Phe	Ile	Gly	Arg	Gln	Ala	Pro	Glu	Glu	Trp	Ser	Val	Gly	Leu	Gly	

	365		370		375
Thr Arg Pro Glu	Glu Trp Gly Leu Lys	Gln Leu Ile Leu His	Gly		
	380	385	390		
Ala Tyr Thr His	Pro Glu Gly Gly Tyr	Asp Met Ala Leu Leu	Leu		
	395	400	405		
Leu Ala Gln Pro	Val Thr Leu Gly Ala	Ser Leu Arg Pro Leu	Cys		
	410	415	420		
Leu Pro Tyr Pro	Asp His His Leu Pro	Asp Gly Glu Arg Gly	Trp		
	425	430	435		
Val Leu Gly Arg	Ala Arg Pro Gly Ala	Gly Ile Ser Ser Leu	Gln		
	440	445	450		
Thr Val Pro Val	Thr Leu Leu Gly Pro	Arg Ala Cys Ser Arg	Leu		
	455	460	465		
His Ala Ala Pro	Gly Gly Asp Gly Ser	Pro Ile Leu Pro Gly	Met		
	470	475	480		
Val Cys Thr Ser	Ala Val Gly Glu Leu	Pro Ser Cys Glu Gly	Leu		
	485	490	495		
Ser Gly Ala Pro	Leu Val His Glu Val	Arg Gly Thr Trp Phe	Leu		
	500	505	510		
Ala Gly Leu His	Ser Phe Gly Asp Ala	Cys Gln Gly Pro Ala	Arg		
	515	520	525		
Pro Ala Val Phe	Thr Ala Leu Pro Ala	Tyr Glu Asp Trp Val	Ser		
	530	535	540		
Ser Leu Asp Trp	Gln Val Tyr Phe Ala	Glu Glu Pro Glu Pro	Glu		
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Ala Glu Pro Gly	Ser Cys Leu Ala Asn	Ile Ser Gln Pro Thr	Ser		
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Cys

<210> 133
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 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 133
 cctgtgctgt gcctcgagcc tgac 24

<210> 134
 <211> 24
 <212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 134

gtgggcagca gttagcaccg cctc 24

<210> 135

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 135

ggctggcatc atcagctttg catcaagctg tgcccaggag gacgc 45

<210> 136

<211> 1998

<212> DNA

<213> Homo sapiens

<400> 136

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ggggcagcct tccaccacgg ggagcccagc tgtcagccgc ctcacaggaa 150
gatgctgcgt cggcggggca gccctggcat ggggtgtcat gtgggtgcag 200
ccctgggagc actgtggttc tgcctcacag gagccctgga ggtccaggtc 250
cctgaagacc cagtgtgtggc actggtgggc accgatgcca ccctgtgctg 300
ctccttctcc cctgagcctg gcttcagcct ggcacagctc aacctcatct 350
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gaccagggca gcgcctatgc caaccgcacg gccctcttcc cggacctgct 450
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 atgccttccg gatgtcatct ctccctgcc caggaatgga agatgtgagg 1900
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 attttgggga aaataaatgt ctttgtaaaa aaaaaaaaaa aaaaaaaaa 1998

<210> 137

<211> 316

<212> PRT

<213> Homo sapiens

<220>

<221> unsure

<222> 233

<223> unknown amino acid

<400> 137

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				20					25					30	
Val	Gln	Val	Pro	Glu	Asp	Pro	Val	Val	Ala	Leu	Val	Gly	Thr	Asp	
				35					40					45	
Ala	Thr	Leu	Cys	Cys	Ser	Phe	Ser	Pro	Glu	Pro	Gly	Phe	Ser	Leu	
				50					55					60	
Ala	Gln	Leu	Asn	Leu	Ile	Trp	Gln	Leu	Thr	Asp	Thr	Lys	Gln	Leu	
				65					70					75	
Val	His	Ser	Phe	Ala	Glu	Gly	Gln	Asp	Gln	Gly	Ser	Ala	Tyr	Ala	
				80					85					90	
Asn	Arg	Thr	Ala	Leu	Phe	Pro	Asp	Leu	Leu	Ala	Gln	Gly	Asn	Ala	
				95					100					105	
Ser	Leu	Arg	Leu	Gln	Arg	Val	Arg	Val	Ala	Asp	Glu	Gly	Ser	Phe	
				110					115					120	
Thr	Cys	Phe	Val	Ser	Ile	Arg	Asp	Phe	Gly	Ser	Ala	Ala	Val	Ser	
				125					130					135	
Leu	Gln	Val	Ala	Ala	Pro	Tyr	Ser	Lys	Pro	Ser	Met	Thr	Leu	Glu	
				140					145					150	
Pro	Asn	Lys	Asp	Leu	Arg	Pro	Gly	Asp	Thr	Val	Thr	Ile	Thr	Cys	
				155					160					165	
Ser	Ser	Tyr	Gln	Gly	Tyr	Pro	Glu	Ala	Glu	Val	Phe	Trp	Gln	Asp	
				170					175					180	
Gly	Gln	Gly	Val	Pro	Leu	Thr	Gly	Asn	Val	Thr	Thr	Ser	Gln	Met	
				185					190					195	
Ala	Asn	Glu	Gln	Gly	Leu	Phe	Asp	Val	His	Ser	Val	Leu	Arg	Val	
				200					205					210	
Val	Leu	Gly	Ala	Asn	Gly	Thr	Tyr	Ser	Cys	Leu	Val	Arg	Asn	Pro	
				215					220					225	
Val	Leu	Gln	Gln	Asp	Ala	His	Xaa	Ser	Val	Thr	Ile	Thr	Gly	Gln	
				230					235					240	
Pro	Met	Thr	Phe	Pro	Pro	Glu	Ala	Leu	Trp	Val	Thr	Val	Gly	Leu	
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Ser	Val	Cys	Leu	Ile	Ala	Leu	Leu	Val	Ala	Leu	Ala	Phe	Val	Cys	
				260					265					270	
Trp	Arg	Lys	Ile	Lys	Gln	Ser	Cys	Glu	Glu	Glu	Asn	Ala	Gly	Ala	
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Glu	Asp	Gln	Asp	Gly	Glu	Gly	Glu	Gly	Ser	Lys	Thr	Ala	Leu	Gln	
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Ala

<210> 138

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 138

ctggcacagc tcaacctcat ctgg 24

<210> 139

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 139

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<210> 140

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 140

ggacacagta tactgaccac 20

<210> 141

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 141

tgccaaccag gcagctgtaa gtgc 24

<210> 142

<211> 24

<212> DNA

<213> Artificial Sequence

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<223> Synthetic oligonucleotide probe

<400> 142
tggaagaaga ggggtggtgat gtgg 24

<210> 143

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 143

cagctgacag acaccaaaca gctggtgcac agtttcaccg aaggc 45

<210> 144

<211> 2336

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> 1620, 1673

<223> unknown base

<400> 144

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taagttctta aatctatgaa gtcgaggag ctttcgctgc ttttgtaggg 150

acttctttcc ttgcttcagc aacatgaggc ttttcttggtg gaacgcggtc 200

ttgactctgt tcgtcacttc tttgattggg gctttgatcc ctgaaccaga 250

agtgaaaatt gaagttctcc agaagccatt catctgccat cgcaagacca 300

aaggagggga tttgatgttg gtccactatg aaggctactt agaaaaggac 350

ggctccttat ttcactccac tcacaaacat aacaatggtc agcccatttg 400

gtttaccctg ggcacccctg aggctctcaa aggttgggac cagggttgta 450

aaggaatgtg ttagaggagag aagagaaagc tcatcattcc tcctgctctg 500

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atttaatat gatctcctgg agattcgaaa tggaccaaga tcccatgaat 600

cattccaaga aatggatctt aatgatgact ggaaactctc taaagatgag 650

gttaaagcat atttaaagaa ggagtttgaa aaacatgggtg cgggtggtgaa 700

tgaaagtcac catgatgctt tgggtggagga tatttttgat aaagaagatg 750

aagacaaaga tgggtttata tctgccagag aatttacata taaacacgat 800

gagttataga gatacatcta cccttttaat atagcactca totttcaaga 850

gagggcagtc atctttaag aacattttat tttatacaa tgttctttct 900
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 gtctacattt tccattttct gtctcatcaa aaactgaagt tagctgggtg 2000
 tgggtggtca tgcttgtaat ccagcactt tgggggcaa ggagggtgga 2050
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 tgtctctact aaaaatacaa aaattagcca ggcgtggtgg tgcacacctg 2150
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 aggcggaggt tgcagtgagc caagattgtg ccactgcact ccagcctggg 2250
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gcagctacta ttgaataaat acctatcctg gatttt 2336

<210> 145

<211> 211

<212> PRT

<213> Homo sapiens

<400> 145

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Ser Leu Ile Gly Ala Leu Ile Pro Glu Pro Glu Val Lys Ile Glu
20 25 30

Val Leu Gln Lys Pro Phe Ile Cys His Arg Lys Thr Lys Gly Gly
35 40 45

Asp Leu Met Leu Val His Tyr Glu Gly Tyr Leu Glu Lys Asp Gly
50 55 60

Ser Leu Phe His Ser Thr His Lys His Asn Asn Gly Gln Pro Ile
65 70 75

Trp Phe Thr Leu Gly Ile Leu Glu Ala Leu Lys Gly Trp Asp Gln
80 85 90

Gly Leu Lys Gly Met Cys Val Gly Glu Lys Arg Lys Leu Ile Ile
95 100 105

Pro Pro Ala Leu Gly Tyr Gly Lys Glu Gly Lys Gly Lys Ile Pro
110 115 120

Pro Glu Ser Thr Leu Ile Phe Asn Ile Asp Leu Leu Glu Ile Arg
125 130 135

Asn Gly Pro Arg Ser His Glu Ser Phe Gln Glu Met Asp Leu Asn
140 145 150

Asp Asp Trp Lys Leu Ser Lys Asp Glu Val Lys Ala Tyr Leu Lys
155 160 165

Lys Glu Phe Glu Lys His Gly Ala Val Val Asn Glu Ser His His
170 175 180

Asp Ala Leu Val Glu Asp Ile Phe Asp Lys Glu Asp Glu Asp Lys
185 190 195

Asp Gly Phe Ile Ser Ala Arg Glu Phe Thr Tyr Lys His Asp Glu
200 205 210

Leu

<210> 146

<211> 26

<212> DNA

<213> Artificial Sequence

tgagcgggac	tccacgggtgg	ccgtgattgt	gggtgcctcc	gtcggggggct	650
tcctggctgt	ggtcatcttg	gtgctgatgg	tgttcaagtg	tgtgaggaga	700
aaaaaagagc	agaagctgag	cacagatgac	ctgaagaccg	aggaggaggg	750
caagacggac	ggtgaaggca	acccggatga	tggcgccaag	tagtggggtg	800
ccggccctgc	agcctcccgt	gtcccgtctc	ctcccctctc	cgccctgtac	850
agtgaccctg	cctgctcgct	cttggtgtgc	ttcccgtgac	ctaggacccc	900
agggccacc	tggggcctcc	tgaacccccg	acttcgtatc	tcccacccctg	950
caccaagagt	gaccactct	cttccatccg	agaaacctgc	catgctcttg	1000
gacgtgtggg	ccctggggag	aggagagaaa	gggctcccac	ctgccagtcc	1050
ctgggggggag	gcaggaggca	catgtgaggg	tcccagaga	gaagggagtg	1100
ggtgggcagg	ggtagaggag	gggcccgtgt	cacctgccca	gtgcttgcc	1150
ggcagtggct	tcagagagga	cctggtgggg	agggagggct	ttcctgtgct	1200
gacagcgctc	cctcaggagg	gccttggcct	ggcacggctg	tgctcctccc	1250
ctgctcccag	cccagagcag	ccatcaggct	ggaggtgacg	atgagttcct	1300
gaaacttgga	ggggcatgtt	aaagggatga	ctgtgcattc	cagggcactg	1350
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gttggtcct	aatcccttag	gactgtggat	gaggccagac	tggaagagca	1500
gctccaggta	gggggccatg	tttcccagcg	gggaccacc	aacagaggcc	1550
agtttcaaag	tcagctgagg	ggctgagggg	tggggctcca	tgggtgaatgc	1600
aggttgctgc	aggctctgcc	ttctccatgg	ggtaaccacc	ctcgcctggg	1650
caggggcagc	caaggctggg	aaatgaggag	gccatgcaca	gggtggggca	1700
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tgcggccacg	ctactcgctc	ctctcccaac	aactcccttc	gtggggacaa	1900
aagtgacaat	tgtaggccag	gcacagtggc	tcacgcctgt	aatcccagca	1950
ctttgggagg	ccaaggcggg	tggattacct	ccatctgttt	agtagaaatg	2000
ggcaaaaacc	catctctact	aaaaatacaa	gaattagctg	ggcgtgggtg	2050

cgtgtgcctg taatcccagc tatttgggag gctgaggcag gagaatcgct 2100
 tgagcccggg aagcagaggt tgcagtgaac tgagatagtg atagtgccac 2150
 tgcaattcag cctgggtgac atagagagac tccatctcaa aaaaaa 2196

<210> 150
 <211> 215
 <212> PRT
 <213> Homo sapiens

<400> 150
 Met His Arg Asp Ala Trp Leu Pro Arg Pro Ala Phe Ser Leu Thr
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 Gly Leu Ser Leu Phe Phe Ser Leu Val Pro Pro Gly Arg Ser Met
 20 25 30
 Glu Val Thr Val Pro Ala Thr Leu Asn Val Leu Asn Gly Ser Asp
 35 40 45
 Ala Arg Leu Pro Cys Thr Phe Asn Ser Cys Tyr Thr Val Asn His
 50 55 60
 Lys Gln Phe Ser Leu Asn Trp Thr Tyr Gln Glu Cys Asn Asn Cys
 65 70 75
 Ser Glu Glu Met Phe Leu Gln Phe Arg Met Lys Ile Ile Asn Leu
 80 85 90
 Lys Leu Glu Arg Phe Gln Asp Arg Val Glu Phe Ser Gly Asn Pro
 95 100 105
 Ser Lys Tyr Asp Val Ser Val Met Leu Arg Asn Val Gln Pro Glu
 110 115 120
 Asp Glu Gly Ile Tyr Asn Cys Tyr Ile Met Asn Pro Pro Asp Arg
 125 130 135
 His Arg Gly His Gly Lys Ile His Leu Gln Val Leu Met Glu Glu
 140 145 150
 Pro Pro Glu Arg Asp Ser Thr Val Ala Val Ile Val Gly Ala Ser
 155 160 165
 Val Gly Gly Phe Leu Ala Val Val Ile Leu Val Leu Met Val Val
 170 175 180
 Lys Cys Val Arg Arg Lys Lys Glu Gln Lys Leu Ser Thr Asp Asp
 185 190 195
 Leu Lys Thr Glu Glu Glu Gly Lys Thr Asp Gly Glu Gly Asn Pro
 200 205 210
 Asp Asp Gly Ala Lys
 215

<210> 151

<211> 524
<212> DNA
<213> Homo sapiens

<220>
<221> unsure
<222> 103, 233
<223> unknown base

<400> 151
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tcctcccttg tagttctcgc cccctcaaat caccttctcc cttagcccac 100
ccnactaaca tctcagtctc tgaaaatgca cagagatgcc tggctacctc 150
gccctgcctt cagcctcacg gggctcagtc tctttttctc tttggtgcca 200
ccaggacgga gcatggaggt ccacagtacc tgnccaccct caacgtcctc 250
aatggctctg acgcccgcct gccctgccct tcaactcctg ctacacagtg 300
aaccacaaac agttctccct gaactggact taccaggagt gcaacaactg 350
ctctgaggag atgttctctc agttccgcat gaagatcatt aacctgaagc 400
tgagagcggt tcaagaccgc gtggagtctc cagggaaccc cagcaagtac 450
gatgtgtcgg tgatgctgag aaacgtgcag ccggaggatg aggggattta 500
caactgctac atcatgaacc cccc 524

<210> 152
<211> 368
<212> DNA
<213> Homo sapiens

<220>
<221> unsure
<222> 56, 123
<223> unknown base

<400> 152
tcacgggggt catctctttt tctcttttgt gccaccagg acggagcatg 50
gaggtncaca tacctgccac cctcaacgtc ctcaatggtt ttgacgcccg 100
cctgcccctgc accttcaact ccngctacac agtgaaccac aaacagttct 150
ccctgaactg gatttaccag gagtgaaca actggctctg aggagatggt 200
cctccagttc ccgcatggaa gatcatttaa cctgaaagct ggaagcgggt 250
ttcaagaacc gogtggaagt ttctcagga accccagcaa gtacgatgtg 300
tcggtgatgc tgagaaacgt gcagccggag gatgagggga tttacaactg 350
ctacatcatg aaccccc 368

<210> 153
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 153
 acggagcatg gaggtccaca gtac 24

<210> 154
 <211> 23
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 154
 gcacgtttct cagcatcacc gac 23

<210> 155
 <211> 50
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 155
 cgcctgcccct gcaccttcaa ctctgctac acagtgaacc acaaacagtt 50

<210> 156
 <211> 2680
 <212> DNA
 <213> Homo sapiens

<400> 156
 tgcggcgacc gtcgtacacc atgggcctcc acctccgccc ctaccgtgtg 50
 gggctgctcc cggatggcct cctgttctctc ttgctgctgc taatgctgct 100
 cgcggaccca gcgctcccgg ccggacgtca cccccagtg gtgctgggtcc 150
 ctggtgattt gggtaaccaa ctggaagcca agctggacaa gccgacagtg 200
 gtgcactacc tctgctccaa gaagaccgaa agctacttca caatctggct 250
 gaacctggaa ctgctgctgc ctgtcatcat tgactgctgg attgacaata 300
 tcaggctggt ttacaacaaa acatccaggg ccacccagtt tcctgatggt 350
 gtggatgtac gtgtccctgg ctttggaag accttctcac tggagttcct 400
 ggaccccagc aaaagcagcg tgggttcta tttccacacc atggtggaga 450
 gccttgtggg ctggggctac acacggggtg aggatgtccg aggggctccc 500

ccccagttcc cgcaggctgt gttccagggg ccctgatttc ctcggtatgtg 2000
ctattggccc caggactgaa gctgcctccc ttcacctgg gactgtgggtt 2050
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atgctgtaaa aaaaaaaaaa aaaaaaaaaa 2680

<210> 157
<211> 412
<212> PRT
<213> Artificial

<400> 157
Met Gly Leu His Leu Arg Pro Tyr Arg Val Gly Leu Leu Pro Asp
1 5 10 15
Gly Leu Leu Phe Leu Leu Leu Leu Leu Met Leu Leu Ala Asp Pro
20 25 30
Ala Leu Pro Ala Gly Arg His Pro Pro Val Val Leu Val Pro Gly
35 40 45
Asp Leu Gly Asn Gln Leu Glu Ala Lys Leu Asp Lys Pro Thr Val
50 55 60
Val His Tyr Leu Cys Ser Lys Lys Thr Glu Ser Tyr Phe Thr Ile
65 70 75
Trp Leu Asn Leu Glu Leu Leu Leu Pro Val Ile Ile Asp Cys Trp
80 85 90
Ile Asp Asn Ile Arg Leu Val Tyr Asn Lys Thr Ser Arg Ala Thr
95 100 105
Gln Phe Pro Asp Gly Val Asp Val Arg Val Pro Gly Phe Gly Lys

110	115	120
Thr Phe Ser Leu Glu Phe Leu Asp Pro	Ser Lys Ser Ser Val Gly	
125	130	135
Ser Tyr Phe His Thr Met Val Glu Ser	Leu Val Gly Trp Gly Tyr	
140	145	150
Thr Arg Gly Glu Asp Val Arg Gly Ala	Pro Tyr Asp Trp Arg Arg	
155	160	165
Ala Pro Asn Glu Asn Gly Pro Tyr Phe	Leu Ala Leu Arg Glu Met	
170	175	180
Ile Glu Glu Met Tyr Gln Leu Tyr Gly	Gly Pro Val Val Leu Val	
185	190	195
Ala His Ser Met Gly Asn Met Tyr Thr	Leu Tyr Phe Leu Gln Arg	
200	205	210
Gln Pro Gln Ala Trp Lys Asp Lys Tyr	Ile Arg Ala Phe Val Ser	
215	220	225
Leu Gly Ala Pro Trp Gly Gly Val Ala	Lys Thr Leu Arg Val Leu	
230	235	240
Ala Ser Gly Asp Asn Asn Arg Ile Pro	Val Ile Gly Pro Leu Lys	
245	250	255
Ile Arg Glu Gln Gln Arg Ser Ala Val	Ser Thr Ser Trp Leu Leu	
260	265	270
Pro Tyr Asn Tyr Thr Trp Ser Pro Glu	Lys Val Phe Val Gln Thr	
275	280	285
Pro Thr Ile Asn Tyr Thr Leu Arg Asp	Tyr Arg Lys Phe Phe Gln	
290	295	300
Asp Ile Gly Phe Glu Asp Gly Trp Leu	Met Arg Gln Asp Thr Glu	
305	310	315
Gly Leu Val Glu Ala Thr Met Pro Pro	Gly Val Gln Leu His Cys	
320	325	330
Leu Tyr Gly Thr Gly Val Pro Thr Pro	Asp Ser Phe Tyr Tyr Glu	
335	340	345
Ser Phe Pro Asp Arg Asp Pro Lys Ile	Cys Phe Gly Asp Gly Asp	
350	355	360
Gly Thr Val Asn Leu Lys Ser Ala Leu	Gln Cys Gln Ala Trp Gln	
365	370	375
Ser Arg Gln Glu His Gln Val Leu Leu	Gln Glu Leu Pro Gly Ser	
380	385	390
Glu His Ile Glu Met Leu Ala Asn Ala	Thr Thr Leu Ala Tyr Leu	
395	400	405

Lys Arg Val Leu Leu Gly Pro
410

<210> 158

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 158

ctggggctac acacggggtg agg 23

<210> 159

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 159

ggtgccgctg cagaaagtag agcg 24

<210> 160

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 160

gccccaaatg aaaacgggcc ctacttctctg gccctccgcg agatg 45

<210> 161

<211> 1512

<212> DNA

<213> Homo sapiens

<400> 161

cgacgcgtg ggcggacgcg tggggcggcg gcagcggcgg cgacggcgac 50

atggagagcg gggcctacgg cgcggccaag gcgggaggct ccttcgacct 100

gcggcgcttc ctgacgcagc cgcaggtggt ggcgcgcgcc gtgtgcttgg 150

tcttcgcctt gatcgtgttc tcttgcattc atggtgaggg ctacagcaat 200

gcccacgagt ctaagcagat gtactgcgtg ttcaaccgca acgaggatgc 250

ctgccgctat ggcagtgcca tcgggggtgct ggccttctctg gcctcggcct 300

tcttcttggg ggtcgacgcg tatttcccc agatcagcaa cgccactgac 350

cgcaagtacc tggtcattgg tgacctgctc ttctcagctc tctggacctt 400

cctgtggttt gttggtttct gtttcctcac caaccagtgg gcagtcacca 450
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 gtgccccatg gctcccagac tctgtctgtg ccgagtgtat tataaaatcg 1450
 tgggggagat gcccggcctg ggatgctgtt tggagacgga ataaatgttt 1500
 tctcattcaa ag 1512

<210> 162

<211> 224

<212> PRT

<213> Homo sapiens

<400> 162

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Asp	Leu	Arg	Arg	Phe	Leu	Thr	Gln	Pro	Gln	Val	Val	Ala	Arg	Ala
				20					25					30

Val	Cys	Leu	Val	Phe	Ala	Leu	Ile	Val	Phe	Ser	Cys	Ile	Tyr	Gly	
				35					40					45	
Glu	Gly	Tyr	Ser	Asn	Ala	His	Glu	Ser	Lys	Gln	Met	Tyr	Cys	Val	
				50					55					60	
Phe	Asn	Arg	Asn	Glu	Asp	Ala	Cys	Arg	Tyr	Gly	Ser	Ala	Ile	Gly	
				65					70					75	
Val	Leu	Ala	Phe	Leu	Ala	Ser	Ala	Phe	Phe	Leu	Val	Val	Asp	Ala	
				80					85					90	
Tyr	Phe	Pro	Gln	Ile	Ser	Asn	Ala	Thr	Asp	Arg	Lys	Tyr	Leu	Val	
				95					100					105	
Ile	Gly	Asp	Leu	Leu	Phe	Ser	Ala	Leu	Trp	Thr	Phe	Leu	Trp	Phe	
				110					115					120	
Val	Gly	Phe	Cys	Phe	Leu	Thr	Asn	Gln	Trp	Ala	Val	Thr	Asn	Pro	
				125					130					135	
Lys	Asp	Val	Leu	Val	Gly	Ala	Asp	Ser	Val	Arg	Ala	Ala	Ile	Thr	
				140					145					150	
Phe	Ser	Phe	Phe	Ser	Ile	Phe	Ser	Trp	Gly	Val	Leu	Ala	Ser	Leu	
				155					160					165	
Ala	Tyr	Gln	Arg	Tyr	Lys	Ala	Gly	Val	Asp	Asp	Phe	Ile	Gln	Asn	
				170					175					180	
Tyr	Val	Asp	Pro	Thr	Pro	Asp	Pro	Asn	Thr	Ala	Tyr	Ala	Ser	Tyr	
				185					190					195	
Pro	Gly	Ala	Ser	Val	Asp	Asn	Tyr	Gln	Gln	Pro	Pro	Phe	Thr	Gln	
				200					205					210	
Asn	Ala	Glu	Thr	Thr	Glu	Gly	Tyr	Gln	Pro	Pro	Pro	Val	Tyr		
				215					220						

<210> 163

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 163

tggtcttcgc cttgatcgtg ttct 24

<210> 164

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 164
gtgtactgag cggcggtag 20

<210> 165
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 165
ctgaaggtga tggctgccct cac 23

<210> 166
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 166
ccaggaggct catgggaaag tcc 23

<210> 167
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 167
ccacgagtct aagcagatgt actgctgtgt caaccgcaac gaggatgcct 50

<210> 168
<211> 3143
<212> DNA
<213> Homo sapiens

<400> 168
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agggtgatca gtgagcagaa ggatgcccggt ggccgaggcc cccaggtgg 100
ctggcgggca gggggacgga ggtgatggcg aggaagcgga gccagagggg 150
atgttcaagg cctgtgagga ctccaagaga aaagcccggg gctacctccg 200
cctggtgccc ctgtttgtgc tgctggccct gctcgtgctg gcttcggcgg 250
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tcttaccgcg cggaatcta gtgccttccg cagtgaacc gccaaagccc 400

agaagatgct caaggagctc atcaccagca cccgcctggg aacttactac 450
aactocagct cegtctattc ctttggggag ggacccctca cctgcttctt 500
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tcccagatct cctcaccgg gcccggtgtg cgggtgcact atggcttgta 1400
caaccagtgc gacccctgcc ctggagagtt cctctgttct gtgaatggac 1450
tctgtgtccc tgctgtgat ggggtcaagg actgccccaa cggcctggat 1500
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tggggggggcc ctcacgctg accgctgggt gataacagct gccactgct 1900
 tccaggagga cagcatggcc tccacggtgc tgtggaccgt gttcctgggc 1950
 aaggtgtggc agaactcgcg ctggcctgga gaggtgtcct tcaaggtgag 2000
 ccgctgctc ctgcacccgt accacgaaga ggacagccat gactacgacg 2050
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 gggacaagta ttctggcggg ggggtggggga gagagcaggc cctgtggtgg 2600
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 aaggtgggga agtctgact ccagggtcct tgccccaccc ctgcctgcca 3050
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 tttggaataa agctgcctga tcaaaaaaaaa aaaaaaaaaa aaa 3143

<210> 169
 <211> 802
 <212> PRT
 <213> Homo sapiens
 <400> 169

Met	Pro	Val	Ala	Glu	Ala	Pro	Gln	Val	Ala	Gly	Gly	Gln	Gly	Asp	
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Gly	Gly	Asp	Gly	Glu	Glu	Ala	Glu	Pro	Glu	Gly	Met	Phe	Lys	Ala	
				20					25					30	
Cys	Glu	Asp	Ser	Lys	Arg	Lys	Ala	Arg	Gly	Tyr	Leu	Arg	Leu	Val	
				35					40					45	
Pro	Leu	Phe	Val	Leu	Leu	Ala	Leu	Leu	Val	Leu	Ala	Ser	Ala	Gly	
				50					55					60	
Val	Leu	Leu	Trp	Tyr	Phe	Leu	Gly	Tyr	Lys	Ala	Glu	Val	Met	Val	
				65					70					75	
Ser	Gln	Val	Tyr	Ser	Gly	Ser	Leu	Arg	Val	Leu	Asn	Arg	His	Phe	
				80					85					90	
Ser	Gln	Asp	Leu	Thr	Arg	Arg	Glu	Ser	Ser	Ala	Phe	Arg	Ser	Glu	
				95					100					105	
Thr	Ala	Lys	Ala	Gln	Lys	Met	Leu	Lys	Glu	Leu	Ile	Thr	Ser	Thr	
				110					115					120	
Arg	Leu	Gly	Thr	Tyr	Tyr	Asn	Ser	Ser	Ser	Val	Tyr	Ser	Phe	Gly	
				125					130					135	
Glu	Gly	Pro	Leu	Thr	Cys	Phe	Phe	Trp	Phe	Ile	Leu	Gln	Ile	Pro	
				140					145					150	
Glu	His	Arg	Arg	Leu	Met	Leu	Ser	Pro	Glu	Val	Val	Gln	Ala	Leu	
				155					160					165	
Leu	Val	Glu	Glu	Leu	Leu	Ser	Thr	Val	Asn	Ser	Ser	Ala	Ala	Val	
				170					175					180	
Pro	Tyr	Arg	Ala	Glu	Tyr	Glu	Val	Asp	Pro	Glu	Gly	Leu	Val	Ile	
				185					190					195	
Leu	Glu	Ala	Ser	Val	Lys	Asp	Ile	Ala	Ala	Leu	Asn	Ser	Thr	Leu	
				200					205					210	
Gly	Cys	Tyr	Arg	Tyr	Ser	Tyr	Val	Gly	Gln	Gly	Gln	Val	Leu	Arg	
				215					220					225	
Leu	Lys	Gly	Pro	Asp	His	Leu	Ala	Ser	Ser	Cys	Leu	Trp	His	Leu	
				230					235					240	
Gln	Gly	Pro	Lys	Asp	Leu	Met	Leu	Lys	Leu	Arg	Leu	Glu	Trp	Thr	
				245					250					255	
Leu	Ala	Glu	Cys	Arg	Asp	Arg	Leu	Ala	Met	Tyr	Asp	Val	Ala	Gly	
				260					265					270	
Pro	Leu	Glu	Lys	Arg	Leu	Ile	Thr	Ser	Val	Tyr	Gly	Cys	Ser	Arg	
				275					280					285	
Gln	Glu	Pro	Val	Val	Glu	Val	Leu	Ala	Ser	Gly	Ala	Ile	Met	Ala	

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Val Val Trp Lys	Lys Gly Leu His Ser Tyr Tyr Asp Pro Phe Val				
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Leu Ser Val Gln	Pro Val Val Phe Gln Ala Cys Glu Val Asn Leu				
	320		325		330
Thr Leu Asp Asn	Arg Leu Asp Ser Gln Gly Val Leu Ser Thr Pro				
	335		340		345
Tyr Phe Pro Ser	Tyr Tyr Ser Pro Gln Thr His Cys Ser Trp His				
	350		355		360
Leu Thr Val Pro	Ser Leu Asp Tyr Gly Leu Ala Leu Trp Phe Asp				
	365		370		375
Ala Tyr Ala Leu	Arg Arg Gln Lys Tyr Asp Leu Pro Cys Thr Gln				
	380		385		390
Gly Gln Trp Thr	Ile Gln Asn Arg Arg Leu Cys Gly Leu Arg Ile				
	395		400		405
Leu Gln Pro Tyr	Ala Glu Arg Ile Pro Val Val Ala Thr Ala Gly				
	410		415		420
Ile Thr Ile Asn	Phe Thr Ser Gln Ile Ser Leu Thr Gly Pro Gly				
	425		430		435
Val Arg Val His	Tyr Gly Leu Tyr Asn Gln Ser Asp Pro Cys Pro				
	440		445		450
Gly Glu Phe Leu	Cys Ser Val Asn Gly Leu Cys Val Pro Ala Cys				
	455		460		465
Asp Gly Val Lys	Asp Cys Pro Asn Gly Leu Asp Glu Arg Asn Cys				
	470		475		480
Val Cys Arg Ala	Thr Phe Gln Cys Lys Glu Asp Ser Thr Cys Ile				
	485		490		495
Ser Leu Pro Lys	Val Cys Asp Gly Gln Pro Asp Cys Leu Asn Gly				
	500		505		510
Ser Asp Glu Glu	Gln Cys Gln Glu Gly Val Pro Cys Gly Thr Phe				
	515		520		525
Thr Phe Gln Cys	Glu Asp Arg Ser Cys Val Lys Lys Pro Asn Pro				
	530		535		540
Gln Cys Asp Gly	Arg Pro Asp Cys Arg Asp Gly Ser Asp Glu Glu				
	545		550		555
His Cys Asp Cys	Gly Leu Gln Gly Pro Ser Ser Arg Ile Val Gly				
	560		565		570
Gly Ala Val Ser	Ser Glu Gly Glu Trp Pro Trp Gln Ala Ser Leu				
	575		580		585

Gln Val Arg Gly	Arg His Ile Cys Gly	Gly Ala Leu Ile Ala Asp	590	595	600
Arg Trp Val Ile	Thr Ala Ala His Cys	Phe Gln Glu Asp Ser Met	605	610	615
Ala Ser Thr Val	Leu Trp Thr Val Phe	Leu Gly Lys Val Trp Gln	620	625	630
Asn Ser Arg Trp	Pro Gly Glu Val Ser	Phe Lys Val Ser Arg Leu	635	640	645
Leu Leu His Pro	Tyr His Glu Glu Asp	Ser His Asp Tyr Asp Val	650	655	660
Ala Leu Leu Gln	Leu Asp His Pro Val	Val Arg Ser Ala Ala Val	665	670	675
Arg Pro Val Cys	Leu Pro Ala Arg Ser	His Phe Phe Glu Pro Gly	680	685	690
Leu His Cys Trp	Ile Thr Gly Trp Gly	Ala Leu Arg Glu Gly Gly	695	700	705
Pro Ile Ser Asn	Ala Leu Gln Lys Val	Asp Val Gln Leu Ile Pro	710	715	720
Gln Asp Leu Cys	Ser Glu Ala Tyr Arg	Tyr Gln Val Thr Pro Arg	725	730	735
Met Leu Cys Ala	Gly Tyr Arg Lys Gly	Lys Lys Asp Ala Cys Gln	740	745	750
Gly Asp Ser Gly	Gly Pro Leu Val Cys	Lys Ala Leu Ser Gly Arg	755	760	765
Trp Phe Leu Ala	Gly Leu Val Ser Trp	Gly Leu Gly Cys Gly Arg	770	775	780
Pro Asn Tyr Phe	Gly Val Tyr Thr Arg	Ile Thr Gly Val Ile Ser	785	790	795
Trp Ile Gln Gln	Val Val Thr		800		

<210> 170
 <211> 1327
 <212> DNA
 <213> Homo sapiens

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 tgcactatgg cttgtacaac cagtcggacc cctgccctgg agagttcctc 200

tgttctgtga atggactctg tgtccctgcc tgtgatgggg tcaaggactg 250
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 gcaaagagga cagcacatgc atctcactgc ccaaggtctg tgatgggcag 350
 cctgattgtc tcaacggcag cgatgaagag cagtgccagg aaggggtgcc 400
 atgtgggaca ttcaccttcc agtgtgagga ccggagctgc gtgaagaagc 450
 ccaacccgca gtgtgatggg cggcccgaact gcagggacgg ctcgatgag 500
 gagcactgtg actgtggcct ccagggcccc tccagccgca ttgttggtgg 550
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 ggggtcgaca catctgtggg ggggccctca tcgctgaccg ctgggtgata 650
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 tgtccttcaa ggtgagccgc ctgctcctgc acccgtaacca cgaagaggac 800
 agccatgact acgacgtggc gctgctgcag ctgcaccacc cgggtggtgcg 850
 ctgggcgcgc gtgcgccccg tctgcctgcc cgcgcgctcc caettcttcg 900
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 ggccccatca gcaacgctct gcagaaagtg gatgtgcagt tgatcccaca 1000
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 ggtccgctgg tgtgcaaggc actcagtggc cgctggttcc tggcggggct 1150
 ggtcagctgg ggccctgggt gtggccggcc taactacttc ggcgctctaca 1200
 ccgcatcac aggtgtgatc agctggatcc agcaagtggg gacctgagga 1250
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 gcaactgcca agcaggggga caagtat 1327

<210> 171

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 171

taacagctgc ccactgcttc cagg 24

<210> 172

<211> 22
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 172
 taatccagca gtgcaggccg gg 22

<210> 173
 <211> 50
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 173
 atggcctcca cgggtgctgtg gaccgtgttc ctgggcaagg tgtggcagaa 50

<210> 174
 <211> 25
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 174
 tgcctatgca ctgaggaggc agaag 25

<210> 175
 <211> 25
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 175
 aggcagggac acagagtcca ttcac 25

<210> 176
 <211> 50
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 176
 agtatgattt gccgtgcacc cagggccagt ggacgatcca gaacaggagg 50

<210> 177
 <211> 1510
 <212> DNA
 <213> Homo sapiens

<400> 177

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 ctocagtccc ccagcccctg gccgagagaa gggctcttacc ggccgggatt 150
 gctggaaaca ccaagaggtg gtttttgttt tttaaaactt ctgtttcttg 200
 ggaggggggtg tggcggggca ggatgagcaa ctccgttcct ctgctctggt 250
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 ccagagggac ggctggaaga taagctccac aaacccaaag ctacacagac 350
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 agcatgaagg atgtacctc tccgtcggcc acagccagcc cttagaagac 450
 tgcagtttca acatgacagc taaaaccttt ttcattcttc acggatggac 500
 gatgagcggg atctttgaaa actggctgca caaactcgtg tcagccctgc 550
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 gccaccagc tttacacgga tgcggtcaat aataccaggg tgggtgggaca 650
 cagcattgcc aggatgctcg actggctgca ggagaaggac gatttttctc 700
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aaaaaaaaaa 1510

<210> 178

<211> 354

<212> PRT

<213> Homo sapiens

<400> 178

Met	Ser	Asn	Ser	Val	Pro	Leu	Leu	Cys	Phe	Trp	Ser	Leu	Cys	Tyr
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Cys	Phe	Ala	Ala	Gly	Ser	Pro	Val	Pro	Phe	Gly	Pro	Glu	Gly	Arg
				20					25					30

Leu	Glu	Asp	Lys	Leu	His	Lys	Pro	Lys	Ala	Thr	Gln	Thr	Glu	Val
				35					40					45

Lys	Pro	Ser	Val	Arg	Phe	Asn	Leu	Arg	Thr	Ser	Lys	Asp	Pro	Glu
				50					55					60

His	Glu	Gly	Cys	Tyr	Leu	Ser	Val	Gly	His	Ser	Gln	Pro	Leu	Glu
				65					70					75

Asp	Cys	Ser	Phe	Asn	Met	Thr	Ala	Lys	Thr	Phe	Phe	Ile	Ile	His
				80					85					90

Gly	Trp	Thr	Met	Ser	Gly	Ile	Phe	Glu	Asn	Trp	Leu	His	Lys	Leu
				95					100					105

Val	Ser	Ala	Leu	His	Thr	Arg	Glu	Lys	Asp	Ala	Asn	Val	Val	Val
				110					115					120

Val	Asp	Trp	Leu	Pro	Leu	Ala	His	Gln	Leu	Tyr	Thr	Asp	Ala	Val
				125					130					135

Asn	Asn	Thr	Arg	Val	Val	Gly	His	Ser	Ile	Ala	Arg	Met	Leu	Asp
				140					145					150

Trp	Leu	Gln	Glu	Lys	Asp	Asp	Phe	Ser	Leu	Gly	Asn	Val	His	Leu
				155					160					165

Ile	Gly	Tyr	Ser	Leu	Gly	Ala	His	Val	Ala	Gly	Tyr	Ala	Gly	Asn
				170					175					180

Phe	Val	Lys	Gly	Thr	Val	Gly	Arg	Ile	Thr	Gly	Leu	Asp	Pro	Ala
				185					190					195

Gly	Pro	Met	Phe	Glu	Gly	Ala	Asp	Ile	His	Lys	Arg	Leu	Ser	Pro
				200					205					210

Asp	Asp	Ala	Asp	Phe	Val	Asp	Val	Leu	His	Thr	Tyr	Thr	Arg	Ser
				215					220					225

Phe	Gly	Leu	Ser	Ile	Gly	Ile	Gln	Met	Pro	Val	Gly	His	Ile	Asp
				230					235					240

Ile	Tyr	Pro	Asn	Gly	Gly	Asp	Phe	Gln	Pro	Gly	Cys	Gly	Leu	Asn
				245					250					255
Asp	Val	Leu	Gly	Ser	Ile	Ala	Tyr	Gly	Thr	Ile	Thr	Glu	Val	Val
				260					265					270
Lys	Cys	Glu	His	Glu	Arg	Ala	Val	His	Leu	Phe	Val	Asp	Ser	Leu
				275					280					285
Val	Asn	Gln	Asp	Lys	Pro	Ser	Phe	Ala	Phe	Gln	Cys	Thr	Asp	Ser
				290					295					300
Asn	Arg	Phe	Lys	Lys	Gly	Ile	Cys	Leu	Ser	Cys	Arg	Lys	Asn	Arg
				305					310					315
Cys	Asn	Ser	Ile	Gly	Tyr	Asn	Ala	Lys	Lys	Met	Arg	Asn	Lys	Arg
				320					325					330
Asn	Ser	Lys	Met	Tyr	Leu	Lys	Thr	Arg	Ala	Gly	Met	Pro	Phe	Arg
				335					340					345
Gly	Asn	Leu	Gln	Ser	Leu	Glu	Cys	Pro						
				350										

<210> 179

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 179

gtgagcatga gcgagccgtc cac 23

<210> 180

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 180

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<210> 181

<211> 44

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 181

ttgactctct ggtgaatcag gacaagccga gttttgcctt ccag 44

<210> 182

<211> 3240
 <212> DNA
 <213> Homo sapiens

<400> 182

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 cgagccacct cttccctccc cccgcttccc tgtcgcgctc cgctggctgg 100
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 caccggaatg ccaattaact agagaccctc cagcccccaa ggggaggatt 3100
 tgggcagaac ctgaggtttt gccatccaca atccctccta cagggcctgg 3150
 ctcacaaaaa gagtgcaca aatgcttcta ttccatagct acggcattgc 3200
 tcagtaagtt gaggtcaaaa ataaaggaat catacatctc 3240

<210> 183
 <211> 713
 <212> PRT
 <213> Homo sapiens

<400> 183
 Met Leu Leu Ala Thr Leu Leu Leu Leu Leu Leu Gly Gly Ala Leu
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 Ala His Pro Asp Arg Ile Ile Phe Pro Asn His Ala Cys Glu Asp
 20 25 30
 Pro Pro Ala Val Leu Leu Glu Val Gln Gly Thr Leu Gln Arg Pro
 35 40 45
 Leu Val Arg Asp Ser Arg Thr Ser Pro Ala Asn Cys Thr Trp Leu
 50 55 60
 Ile Leu Gly Ser Lys Glu Gln Thr Val Thr Ile Arg Phe Gln Lys
 65 70 75
 Leu His Leu Ala Cys Gly Ser Glu Arg Leu Thr Leu Arg Ser Pro
 80 85 90
 Leu Gln Pro Leu Ile Ser Leu Cys Glu Ala Pro Pro Ser Pro Leu
 95 100 105
 Gln Leu Pro Gly Gly Asn Val Thr Ile Thr Tyr Ser Tyr Ala Gly
 110 115 120
 Ala Arg Ala Pro Met Gly Gln Gly Phe Leu Leu Ser Tyr Ser Gln
 125 130 135
 Asp Trp Leu Met Cys Leu Gln Glu Glu Phe Gln Cys Leu Asn His
 140 145 150
 Arg Cys Val Ser Ala Val Gln Arg Cys Asp Gly Val Asp Ala Cys
 155 160 165
 Gly Asp Gly Ser Asp Glu Ala Gly Cys Ser Ser Asp Pro Phe Pro

	170		175		180
Gly Leu Thr Pro Arg Pro Val Pro Ser Leu Pro Cys Asn Val Thr	185		190		195
Leu Glu Asp Phe Tyr Gly Val Phe Ser Ser Pro Gly Tyr Thr His	200		205		210
Leu Ala Ser Val Ser His Pro Gln Ser Cys His Trp Leu Leu Asp	215		220		225
Pro His Asp Gly Arg Arg Leu Ala Val Arg Phe Thr Ala Leu Asp	230		235		240
Leu Gly Phe Gly Asp Ala Val His Val Tyr Asp Gly Pro Gly Pro	245		250		255
Pro Glu Ser Ser Arg Leu Leu Arg Ser Leu Thr His Phe Ser Asn	260		265		270
Gly Lys Ala Val Thr Val Glu Thr Leu Ser Gly Gln Ala Val Val	275		280		285
Ser Tyr His Thr Val Ala Trp Ser Asn Gly Arg Gly Phe Asn Ala	290		295		300
Thr Tyr His Val Arg Gly Tyr Cys Leu Pro Trp Asp Arg Pro Cys	305		310		315
Gly Leu Gly Ser Gly Leu Gly Ala Gly Glu Gly Leu Gly Glu Arg	320		325		330
Cys Tyr Ser Glu Ala Gln Arg Cys Asp Gly Ser Trp Asp Cys Ala	335		340		345
Asp Gly Thr Asp Glu Glu Asp Cys Pro Gly Cys Pro Pro Gly His	350		355		360
Phe Pro Cys Gly Ala Ala Gly Thr Ser Gly Ala Thr Ala Cys Tyr	365		370		375
Leu Pro Ala Asp Arg Cys Asn Tyr Gln Thr Phe Cys Ala Asp Gly	380		385		390
Ala Asp Glu Arg Arg Cys Arg His Cys Gln Pro Gly Asn Phe Arg	395		400		405
Cys Arg Asp Glu Lys Cys Val Tyr Glu Thr Trp Val Cys Asp Gly	410		415		420
Gln Pro Asp Cys Ala Asp Gly Ser Asp Glu Trp Asp Cys Ser Tyr	425		430		435
Val Leu Pro Arg Lys Val Ile Thr Ala Ala Val Ile Gly Ser Leu	440		445		450
Val Cys Gly Leu Leu Leu Val Ile Ala Leu Gly Cys Thr Cys Lys	455		460		465

Leu Tyr Ala Ile	Arg Thr Gln Glu Tyr	Ser Ile Phe Ala Pro Leu	470	475	480
Ser Arg Met Glu	Ala Glu Ile Val Gln	Gln Gln Ala Pro Pro Ser	485	490	495
Tyr Gly Gln Leu	Ile Ala Gln Gly Ala	Ile Pro Pro Val Glu Asp	500	505	510
Phe Pro Thr Glu	Asn Pro Asn Asp Asn	Ser Val Leu Gly Asn Leu	515	520	525
Arg Ser Leu Leu	Gln Ile Leu Arg Gln	Asp Met Thr Pro Gly Gly	530	535	540
Gly Pro Gly Ala	Arg Arg Arg Gln Arg	Gly Arg Leu Met Arg Arg	545	550	555
Leu Val Arg Arg	Leu Arg Arg Trp Gly	Leu Leu Pro Arg Thr Asn	560	565	570
Thr Pro Ala Arg	Ala Ser Glu Ala Arg	Ser Gln Val Thr Pro Ser	575	580	585
Ala Ala Pro Leu	Glu Ala Leu Asp Gly	Gly Thr Gly Pro Ala Arg	590	595	600
Glu Gly Gly Ala	Val Gly Gly Gln Asp	Gly Glu Gln Ala Pro Pro	605	610	615
Leu Pro Ile Lys	Ala Pro Leu Pro Ser	Ala Ser Thr Ser Pro Ala	620	625	630
Pro Thr Thr Val	Pro Glu Ala Pro Gly	Pro Leu Pro Ser Leu Pro	635	640	645
Leu Glu Pro Ser	Leu Leu Ser Gly Val	Val Gln Ala Leu Arg Gly	650	655	660
Arg Leu Leu Pro	Ser Leu Gly Pro Pro	Gly Pro Thr Arg Ser Pro	665	670	675
Pro Gly Pro His	Thr Ala Val Leu Ala	Leu Glu Asp Glu Asp Asp	680	685	690
Val Leu Leu Val	Pro Leu Ala Glu Pro	Gly Val Trp Val Ala Glu	695	700	705
Ala Glu Asp Glu	Pro Leu Leu Thr		710		

<210> 184

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 184
ggctgtcact gtggagacac 20

<210> 185
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 185
gcaaggtcat tacagctg 18

<210> 186
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 186
agaacatagg agcagtccca ctc 23

<210> 187
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 187
tgcttgctgc tgcacaatct cag 23

<210> 188
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 188
ggctattgct tgccttgga cagaccctgt ggcttaggct ctggc 45

<210> 189
<211> 663
<212> DNA
<213> Homo sapiens

<400> 189
cgagctgggc gagaagtagg ggagggcggt gtcgccgc ggtggcggtt 50
gctatcgctt cgcagaacct actcaggcag ccagctgaga agagttgagg 100
gaaagtgctg ctgctgggtc tgcagacgcg atggataacg tgcagccgaa 150

aataaaacat cgcccccttct gcttcagtgt gaaaggccac gtgaagatgc 200
 tgcggtctggc actaactgtg acatctatga ccttttttat catcgacaaa 250
 gccctgaac catatattgt tatcactgga tttgaagtca ccgttatctt 300
 atttttcata ctttttatatg tactcagact tgatogatta atgaagtggg 350
 ttttttgccc tttgcttgat attatcaact cactggtaac aacagtattc 400
 atgctcatcg tatctgtgtt ggcaactgata ccagaaacca caacattgac 450
 agttgggtgga ggggtgtttg cacttgtagc agcagtatgc tgtcttgccg 500
 acggggccct tatttaccgg aagcttctgt tcaatcccag cggtccttac 550
 cagaaaaagc ctgtgcatga aaaaaaagaa gttttgtaat tttatattac 600
 tttttagttt gatactaagt attaaacata tttctgtatt cttccaaaaa 650
 aaaaaaaaaa aaa 663

<210> 190
 <211> 152
 <212> PRT
 <213> Homo sapiens

<400> 190
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 Ser Val Lys Gly His Val Lys Met Leu Arg Leu Ala Leu Thr Val
 20 25 30
 Thr Ser Met Thr Phe Phe Ile Ile Ala Gln Ala Pro Glu Pro Tyr
 35 40 45
 Ile Val Ile Thr Gly Phe Glu Val Thr Val Ile Leu Phe Phe Ile
 50 55 60
 Leu Leu Tyr Val Leu Arg Leu Asp Arg Leu Met Lys Trp Leu Phe
 65 70 75
 Trp Pro Leu Leu Asp Ile Ile Asn Ser Leu Val Thr Thr Val Phe
 80 85 90
 Met Leu Ile Val Ser Val Leu Ala Leu Ile Pro Glu Thr Thr Thr
 95 100 105
 Leu Thr Val Gly Gly Gly Val Phe Ala Leu Val Thr Ala Val Cys
 110 115 120
 Cys Leu Ala Asp Gly Ala Leu Ile Tyr Arg Lys Leu Leu Phe Asn
 125 130 135
 Pro Ser Gly Pro Tyr Gln Lys Lys Pro Val His Glu Lys Lys Glu
 140 145 150

Val Leu

<210> 191
<211> 495
<212> DNA
<213> Homo sapiens

<220>
<221> unsure
<222> 78, 212, 234, 487
<223> unknown base

<400> 191
gggcgagaag taggggaggg cgtgttccgc cgcggtggcg gttgctatcg 50
ttttgcagaa cctactcagg cagccagntg agaagagttg agggaaagtg 100
ctgctgctgg gtctgcagac gcgatggata acgtgcagcc gaaaataaaa 150
catcgcccct tctgcttcag tgtgaaaggc cacgtgaaga tgctgcggt 200
ggcactaact gngacatcta tgacctttt tatnatcgca caagcccctg 250
aaccatatat tgttatcact ggatttgaag tcaccgttat cttatttttc 300
atacttttat atgtactcag acttgatcga ttaatgaagt ggttattttg 350
gcctttgctt gatattatca actcactggt aacaacagta ttcattgctca 400
tcgtatctgt gttggcactg ataccagaaa ccacaacatt gacagttggt 450
ggaggggtgt ttgcacttgt gacagcagta tgctgtnttg ccgac 495

<210> 192
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 192
cgttttgcag aacctactca ggcag 25

<210> 193
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 193
cctccaccaa ctgtcaatgt tgtgg 25

<210> 194
<211> 40

<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 194
aaagtgctgc tgctgggtct gcagacgcga tggataacgt 40

<210> 195
<211> 1879
<212> DNA
<213> Homo sapien

<400> 195
cagccccgcg cgccggccga gtcgctgagc cgcggtgcc ggacgggacg 50
ggacgggcta ggctgggcgc gccccccggg ccccgccgtg ggcattgggcg 100
cactggcccc ggctgctgct ctgcctctgc tggcccagtg gctcctgcgc 150
gccgccccgg agctggcccc cgcgcccttc acgtgcccc tccgggtggc 200
cgcggccacg aaccgcgtag ttgcgccac cccgggaccc gggaccctg 250
ccgagcgcca cgccgacggc ttggcgctcg ccttgagacc tgccctggcg 300
tcccccgcg ggcgcgcca cttcttggcc atggtagaca acctgcaggg 350
ggactctggc cgcggtact acctggagat gctgatcggg accccccgc 400
agaagctaca gattctcgtt gacactcgaa gcagtaactt tgccgtggca 450
ggaacccgc actcctacat agacacgtac ttgacacag agaggtctag 500
cacataccgc tccaagggt ttgacgtcac agtgaagtac acacaaggaa 550
gctggacggg cttcgttggg gaagacctg tcaccatccc caaaggcttc 600
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acacaagcaa acatccccaa cgttttctcc atgcagatgt gtggagccgg 800
cttgcccgtt gctggatctg ggaccaacgg aggtagtctt gtcttgggtg 850
gaattgaacc aagtttgtat aaaggagaca tctgttatac cctattaag 900
gaagagtggg actaccagat agaaattctg aaattggaaa ttggaggcca 950
aagccttaat ctggactgca gagagtataa cgcagacaag gccatcgtgg 1000
acagtggcac cacgctgctg cgctgcccc agaaggtggt tgatgcggtg 1050
gtggaagctg tggccgcgc atctctgatt ccagaattct ctgatggttt 1100

Gln	Ile	Leu	Val	Asp	Thr	Gly	Ser	Ser	Asn	Phe	Ala	Val	Ala	Gly	
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Thr	Pro	His	Ser	Tyr	Ile	Asp	Thr	Tyr	Phe	Asp	Thr	Glu	Arg	Ser	
				125					130					135	
Ser	Thr	Tyr	Arg	Ser	Lys	Gly	Phe	Asp	Val	Thr	Val	Lys	Tyr	Thr	
				140					145					150	
Gln	Gly	Ser	Trp	Thr	Gly	Phe	Val	Gly	Glu	Asp	Leu	Val	Thr	Ile	
				155					160					165	
Pro	Lys	Gly	Phe	Asn	Thr	Ser	Phe	Leu	Val	Asn	Ile	Ala	Thr	Ile	
				170					175					180	
Phe	Glu	Ser	Glu	Asn	Phe	Phe	Leu	Pro	Gly	Ile	Lys	Trp	Asn	Gly	
				185					190					195	
Ile	Leu	Gly	Leu	Ala	Tyr	Ala	Thr	Leu	Ala	Lys	Pro	Ser	Ser	Ser	
				200					205					210	
Leu	Glu	Thr	Phe	Phe	Asp	Ser	Leu	Val	Thr	Gln	Ala	Asn	Ile	Pro	
				215					220					225	
Asn	Val	Phe	Ser	Met	Gln	Met	Cys	Gly	Ala	Gly	Leu	Pro	Val	Ala	
				230					235					240	
Gly	Ser	Gly	Thr	Asn	Gly	Gly	Ser	Leu	Val	Leu	Gly	Gly	Ile	Glu	
				245					250					255	
Pro	Ser	Leu	Tyr	Lys	Gly	Asp	Ile	Trp	Tyr	Thr	Pro	Ile	Lys	Glu	
				260					265					270	
Glu	Trp	Tyr	Tyr	Gln	Ile	Glu	Ile	Leu	Lys	Leu	Glu	Ile	Gly	Gly	
				275					280					285	
Gln	Ser	Leu	Asn	Leu	Asp	Cys	Arg	Glu	Tyr	Asn	Ala	Asp	Lys	Ala	
				290					295					300	
Ile	Val	Asp	Ser	Gly	Thr	Thr	Leu	Leu	Arg	Leu	Pro	Gln	Lys	Val	
				305					310					315	
Phe	Asp	Ala	Val	Val	Glu	Ala	Val	Ala	Arg	Ala	Ser	Leu	Ile	Pro	
				320					325					330	
Glu	Phe	Ser	Asp	Gly	Phe	Trp	Thr	Gly	Ser	Gln	Leu	Ala	Cys	Trp	
				335					340					345	
Thr	Asn	Ser	Glu	Thr	Pro	Trp	Ser	Tyr	Phe	Pro	Lys	Ile	Ser	Ile	
				350					355					360	
Tyr	Leu	Arg	Asp	Glu	Asn	Ser	Ser	Arg	Ser	Phe	Arg	Ile	Thr	Ile	
				365					370					375	
Leu	Pro	Gln	Leu	Tyr	Ile	Gln	Pro	Met	Met	Gly	Ala	Gly	Leu	Asn	
				380					385					390	
Tyr	Glu	Cys	Tyr	Arg	Phe	Gly	Ile	Ser	Pro	Ser	Thr	Asn	Ala	Leu	

	395		400		405
Val Ile Gly Ala Thr Val Met Glu Gly Phe Tyr Val Ile Phe Asp					
	410		415		420
Arg Ala Gln Lys Arg Val Gly Phe Ala Ala Ser Pro Cys Ala Glu					
	425		430		435
Ile Ala Gly Ala Ala Val Ser Glu Ile Ser Gly Pro Phe Ser Thr					
	440		445		450
Glu Asp Val Ala Ser Asn Cys Val Pro Ala Gln Ser Leu Ser Glu					
	455		460		465
Pro Ile Leu Trp Ile Val Ser Tyr Ala Leu Met Ser Val Cys Gly					
	470		475		480
Ala Ile Leu Leu Val Leu Ile Val Leu Leu Leu Leu Pro Phe Arg					
	485		490		495
Cys Gln Arg Arg Pro Arg Asp Pro Glu Val Val Asn Asp Glu Ser					
	500		505		510
Ser Leu Val Arg His Arg Trp Lys					
	515				

<210> 197
 <211> 21
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 197
 cgcagaagct acagattctc g 21

<210> 198
 <211> 19
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 198
 ggaaattgga ggccaaagc 19

<210> 199
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 199
 ggatgtagcc agcaactgtg 20

<210> 200
 <211> 19
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 200
 gccttggtc gttctcttc 19

<210> 201
 <211> 18
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 201
 ggtcctgtgc ctggatgg 18

<210> 202
 <211> 22
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 202
 gacaagacta cctccgttgg tc 22

<210> 203
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 203
 tgatgcacag ttcagcacct gttg 24

<210> 204
 <211> 47
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 204
 cgctccaagg gctttgacgt cacagtgaag tacacacaag gaagctg 47

<210> 205
 <211> 1939
 <212> DNA

<213> Homo sapiens

<400> 205

cgctccgcc ttcggaggct gacgcgccc ggcccggttc caggcctgtg 50
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gggcgggagc cgggaggcgc ggccggcatg gaggcgctgc tgctgggcgc 150
ggggttgctg ctgggcgctt acgtgcttgt ctactacaac ctggtgaagg 200
ccccgccgtg cggcggcatg ggcaacctgc ggggcgcac ggccgtggtc 250
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 aattaccccc atgttaatga agcggaaatta ggctcccgag ctaagggact 1700
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 cagggcaggg cagctggtat cgaggtgccc catgggagta aggggacgcc 1850
 ttccgggchg atgcagggtt ggggtcatct gtatctgaag cccctcggaa 1900
 taaagcgcgt tgaccgcca aaaaaaaaaa aaaaaaaaaa 1939

<210> 206
 <211> 377
 <212> PRT
 <213> Homo sapiens

<400> 206
 Met Glu Ala Leu Leu Leu Gly Ala Gly Leu Leu Leu Gly Ala Tyr
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 Val Leu Val Tyr Tyr Asn Leu Val Lys Ala Pro Pro Cys Gly Gly
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 Met Gly Asn Leu Arg Gly Arg Thr Ala Val Val Thr Gly Ala Asn
 35 40 45
 Ser Gly Ile Gly Lys Met Thr Ala Leu Glu Leu Ala Arg Arg Gly
 50 55 60
 Ala Arg Val Val Leu Ala Cys Arg Ser Gln Glu Arg Gly Glu Ala
 65 70 75
 Ala Ala Phe Asp Leu Arg Gln Glu Ser Gly Asn Asn Glu Val Ile
 80 85 90
 Phe Met Ala Leu Asp Leu Ala Ser Leu Ala Ser Val Arg Ala Phe
 95 100 105
 Ala Thr Ala Phe Leu Ser Ser Glu Pro Arg Leu Asp Ile Leu Ile
 110 115 120
 His Asn Ala Gly Ile Ser Ser Cys Gly Arg Thr Arg Glu Ala Phe
 125 130 135
 Asn Leu Leu Leu Arg Val Asn His Ile Gly Pro Phe Leu Leu Thr
 140 145 150

His	Leu	Leu	Leu	Pro	Cys	Leu	Lys	Ala	Cys	Ala	Pro	Ser	Arg	Val	155	160	165
Val	Val	Val	Ala	Ser	Ala	Ala	His	Cys	Arg	Gly	Arg	Leu	Asp	Phe	170	175	180
Lys	Arg	Leu	Asp	Arg	Pro	Val	Val	Gly	Trp	Arg	Gln	Glu	Leu	Arg	185	190	195
Ala	Tyr	Ala	Asp	Thr	Lys	Leu	Ala	Asn	Val	Leu	Phe	Ala	Arg	Glu	200	205	210
Leu	Ala	Asn	Gln	Leu	Glu	Ala	Thr	Gly	Val	Thr	Cys	Tyr	Ala	Ala	215	220	225
His	Pro	Gly	Pro	Val	Asn	Ser	Glu	Leu	Phe	Leu	Arg	His	Val	Pro	230	235	240
Gly	Trp	Leu	Arg	Pro	Leu	Leu	Arg	Pro	Leu	Ala	Trp	Leu	Val	Leu	245	250	255
Arg	Ala	Pro	Arg	Gly	Gly	Ala	Gln	Thr	Pro	Leu	Tyr	Cys	Ala	Leu	260	265	270
Gln	Glu	Gly	Ile	Glu	Pro	Leu	Ser	Gly	Arg	Tyr	Phe	Ala	Asn	Cys	275	280	285
His	Val	Glu	Glu	Val	Pro	Pro	Ala	Ala	Arg	Asp	Asp	Arg	Ala	Ala	290	295	300
His	Arg	Leu	Trp	Glu	Ala	Ser	Lys	Arg	Leu	Ala	Gly	Leu	Gly	Pro	305	310	315
Gly	Glu	Asp	Ala	Glu	Pro	Asp	Glu	Asp	Pro	Gln	Ser	Glu	Asp	Ser	320	325	330
Glu	Ala	Pro	Ser	Ser	Leu	Ser	Thr	Pro	His	Pro	Glu	Glu	Pro	Thr	335	340	345
Val	Ser	Gln	Pro	Tyr	Pro	Ser	Pro	Gln	Ser	Ser	Pro	Asp	Leu	Ser	350	355	360
Lys	Met	Thr	His	Arg	Ile	Gln	Ala	Lys	Val	Glu	Pro	Glu	Ile	Gln	365	370	375

Leu Ser

<210> 207

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 207

cttcatggcc ttggacttgg ccag 24

<210> 208
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 208
 acgccagtgg cctcaagctg gttg 24

<210> 209
 <211> 45
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 209
 ctttctgagc tctgagccac ggttgacat cctcatccac aatgc 45

<210> 210
 <211> 3716
 <212> DNA
 <213> Homo sapiens

<400> 210
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 acccccagga ccagctgttc cagggccctg gccctgccag gatgagctgc 150
 caagcctcag gccagccacc tcccaccatc cgctgggtgc tgaatgggca 200
 gccctgagc atggtgcccc cagaccaca ccacctcctg cctgatggga 250
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 gccctgtcca cagacctggg tgtctacaca tgtgaggcca gcaaccggct 350
 tggcacggca gtcagcagag gcgctcggct gtctgtggct gtctccggg 400
 aggatttcca gatccagcct cgggacatgg tggctgtggt gggtagcag 450
 ttactctgg aatgtgggcc gccctggggc caccagagc ccacagtctc 500
 atggtggaaa gatgggaaac ccttggccct ccagcccga aggcacacag 550
 tgtccggggg gtccctgctg atggcaagag cagagaagag tgacgaagg 600
 acctacatgt gtgtggccac caacagcgca ggacatagg agagccgcgc 650
 agcccggtt tccatccagg agccccagga ctacacggag cctgtggagc 700
 ttctggctgt gcgaattcag ctggaaaatg tgacactgct gaaccggat 750

caccacagggc tccctcctcc atcctgctgc cagcagcccc catccccatc 2250
 cttagcccct gcagtccccc tagccccag gcctcttccc tctctggccc 2300
 cagcccagct tccagtcgcc tgtccagctc ctactgtca tccctggggg 2350
 aggatcaaga cagcgtgctg acccctgagg aggtagccct gtgcttgga 2400
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 ggctccttca cccccacca cctatgggta catcagcgtc ccaacagcct 2500
 cagagtccac ggacatgggc aggactggag gaggggtggg gcccaagggg 2550
 ggagtcttgc tgtgccacc tcggccctgc ctcaccccca cccccagoga 2600
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aaaaaaaaaa aaaaaa 3716

<210> 211

<211> 985

<212> PRT

<213> Homo sapiens

<400> 211

Met	Gly	Gly	Met	Ala	Gln	Asp	Ser	Pro	Pro	Gln	Ile	Leu	Val	His
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Pro	Gln	Asp	Gln	Leu	Phe	Gln	Gly	Pro	Gly	Pro	Ala	Arg	Met	Ser
			20						25					30

Cys	Gln	Ala	Ser	Gly	Gln	Pro	Pro	Pro	Thr	Ile	Arg	Trp	Leu	Leu
				35					40					45

Asn	Gly	Gln	Pro	Leu	Ser	Met	Val	Pro	Pro	Asp	Pro	His	His	Leu
				50					55					60

Leu	Pro	Asp	Gly	Thr	Leu	Leu	Leu	Leu	Gln	Pro	Pro	Ala	Arg	Gly
				65					70					75

His	Ala	His	Asp	Gly	Gln	Ala	Leu	Ser	Thr	Asp	Leu	Gly	Val	Tyr
				80					85					90

Thr	Cys	Glu	Ala	Ser	Asn	Arg	Leu	Gly	Thr	Ala	Val	Ser	Arg	Gly
				95					100					105

Ala	Arg	Leu	Ser	Val	Ala	Val	Leu	Arg	Glu	Asp	Phe	Gln	Ile	Gln
				110					115					120

Pro	Arg	Asp	Met	Val	Ala	Val	Val	Gly	Glu	Gln	Phe	Thr	Leu	Glu
				125					130					135

Cys	Gly	Pro	Pro	Trp	Gly	His	Pro	Glu	Pro	Thr	Val	Ser	Trp	Trp
				140					145					150

Lys	Asp	Gly	Lys	Pro	Leu	Ala	Leu	Gln	Pro	Gly	Arg	His	Thr	Val
				155					160					165

Ser	Gly	Gly	Ser	Leu	Leu	Met	Ala	Arg	Ala	Glu	Lys	Ser	Asp	Glu
				170					175					180

Gly	Thr	Tyr	Met	Cys	Val	Ala	Thr	Asn	Ser	Ala	Gly	His	Arg	Glu
				185					190					195

Ser	Arg	Ala	Ala	Arg	Val	Ser	Ile	Gln	Glu	Pro	Gln	Asp	Tyr	Thr
				200					205					210

Glu	Pro	Val	Glu	Leu	Leu	Ala	Val	Arg	Ile	Gln	Leu	Glu	Asn	Val
				215					220					225

Thr	Leu	Leu	Asn	Pro	Asp	Pro	Ala	Glu	Gly	Pro	Lys	Pro	Arg	Pro
				230					235					240

Ala Val Trp Leu Ser Trp Lys Val Ser Gly Pro Ala Ala Pro Ala	245	250	255
Gln Ser Tyr Thr Ala Leu Phe Arg Thr Gln Thr Ala Pro Gly Gly	260	265	270
Gln Gly Ala Pro Trp Ala Glu Glu Leu Leu Ala Gly Trp Gln Ser	275	280	285
Ala Glu Leu Gly Gly Leu His Trp Gly Gln Asp Tyr Glu Phe Lys	290	295	300
Val Arg Pro Ser Ser Gly Arg Ala Arg Gly Pro Asp Ser Asn Val	305	310	315
Leu Leu Leu Arg Leu Pro Glu Lys Val Pro Ser Ala Pro Pro Gln	320	325	330
Glu Val Thr Leu Lys Pro Gly Asn Gly Thr Val Phe Val Ser Trp	335	340	345
Val Pro Pro Pro Ala Glu Asn His Asn Gly Ile Ile Arg Gly Tyr	350	355	360
Gln Val Trp Ser Leu Gly Asn Thr Ser Leu Pro Pro Ala Asn Trp	365	370	375
Thr Val Val Gly Glu Gln Thr Gln Leu Glu Ile Ala Thr His Met	380	385	390
Pro Gly Ser Tyr Cys Val Gln Val Ala Ala Val Thr Gly Ala Gly	395	400	405
Ala Gly Glu Pro Ser Arg Pro Val Cys Leu Leu Leu Glu Gln Ala	410	415	420
Met Glu Arg Ala Thr Gln Glu Pro Ser Glu His Gly Pro Trp Thr	425	430	435
Leu Glu Gln Leu Arg Ala Thr Leu Lys Arg Pro Glu Val Ile Ala	440	445	450
Thr Cys Gly Val Ala Leu Trp Leu Leu Leu Leu Gly Thr Ala Val	455	460	465
Cys Ile His Arg Arg Arg Arg Ala Arg Val His Leu Gly Pro Gly	470	475	480
Leu Tyr Arg Tyr Thr Ser Glu Asp Ala Ile Leu Lys His Arg Met	485	490	495
Asp His Ser Asp Ser Gln Trp Leu Ala Asp Thr Trp Arg Ser Thr	500	505	510
Ser Gly Ser Arg Asp Leu Ser Ser Ser Ser Ser Leu Ser Ser Arg	515	520	525
Leu Gly Ala Asp Ala Arg Asp Pro Leu Asp Cys Arg Arg Ser Leu			

Gly	Val	Gly	Pro	Lys	Gly	Gly	Val	Leu	Leu	Cys	Pro	Pro	Arg	Pro	
				830					835					840	
Cys	Leu	Thr	Pro	Thr	Pro	Ser	Glu	Gly	Ser	Leu	Ala	Asn	Gly	Trp	
				845					850					855	
Gly	Ser	Ala	Ser	Glu	Asp	Asn	Ala	Ala	Ser	Ala	Arg	Ala	Ser	Leu	
				860					865					870	
Val	Ser	Ser	Ser	Asp	Gly	Ser	Phe	Leu	Ala	Asp	Ala	His	Phe	Ala	
				875					880					885	
Arg	Ala	Leu	Ala	Val	Ala	Val	Asp	Ser	Phe	Gly	Phe	Gly	Leu	Glu	
				890					895					900	
Pro	Arg	Glu	Ala	Asp	Cys	Val	Phe	Ile	Asp	Ala	Ser	Ser	Pro	Pro	
				905					910					915	
Ser	Pro	Arg	Asp	Glu	Ile	Phe	Leu	Thr	Pro	Asn	Leu	Ser	Leu	Pro	
				920					925					930	
Leu	Trp	Glu	Trp	Arg	Pro	Asp	Trp	Leu	Glu	Asp	Met	Glu	Val	Ser	
				935					940					945	
His	Thr	Gln	Arg	Leu	Gly	Arg	Gly	Met	Pro	Pro	Trp	Pro	Pro	Asp	
				950					955					960	
Ser	Gln	Ile	Ser	Ser	Gln	Arg	Ser	Gln	Leu	His	Cys	Arg	Met	Pro	
				965					970					975	
Lys	Ala	Gly	Ala	Ser	Pro	Val	Asp	Tyr	Ser						
				980					985						

<210> 212

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 212

gaagggacct acatgtgtgt ggcc 24

<210> 213

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 213

actgaccttc cagctgagcc acac 24

<210> 214

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 214

aggactacac ggagcctgtg gagctttctgg ctgtgcgaat tcagctggaa 50

<210> 215

<211> 2749

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> 1869, 1887

<223> unknown base

<400> 215

ctcccacggt gtccagcgcc cagaatgcgg cttctgggtcc tgctatgggg 50

ttgcctgctg ctcccaggtt atgaagccct ggagggccca gaggaaatca 100

gcgggttcga aggggacact gtgtccctgc agtgcaccta cagggaagag 150

ctgagggacc accggaagta ctggtgcagg aagggtggga tcctcttctc 200

tcgctgctct ggcaccatct atgcagaaga agaaggccag gagacaatga 250

agggcaggggt gtccatccgt gacagccgcc aggagctctc gctcattgtg 300

accctgtgga acctcaccct gcaagacgct ggggagtact ggtgtgggg 350

cgaaaaacgg ggccccgatg agtctttact gatctctctg ttctgttttc 400

caggaccctg ctgtcctccc tccccttctc ccaccttcca gcctctggct 450

acaacacgcc tgcagcccaa ggcaaaagct cagcaaacc agccccag 500

attgacttct cctgggtctt acccggcagc caccacagcc aagcagggga 550

agacaggggc tgaggcccct ccattgccag ggacttccca gtacgggcac 600

gaaaggactt ctcagtacac aggaacctct cctcaccag cgacctctcc 650

tcctgcaggg agtcccgcc ccccatgca gctggactcc acctcagcag 700

aggacaccag tccagctctc agcagtggca gctctaagcc cagggtgtcc 750

atcccgatgg tccgcatact ggccccagtc ctggtgctgc tgagccttct 800

gtcagccgca ggccatgatc cttctgcag ccacctgctc ctgtggagaa 850

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tcacgcttga ctgcggagga aaaggaagcc ccttcccagg cccctgaggg 950

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tctcgaagtt tgtctcagcg tagggcagga ggccctcctg gccaggccag 1050
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 gaccttttta taaataaaat gttcatcagc tgcataaaaa aaaaaaaaa 2749

<210> 216

<211> 332

<212> PRT

<213> Homo sapiens

<400> 216

Met	Arg	Leu	Leu	Val	Leu	Leu	Trp	Gly	Cys	Leu	Leu	Leu	Pro	Gly	1	5	10	15
Tyr	Glu	Ala	Leu	Glu	Gly	Pro	Glu	Glu	Ile	Ser	Gly	Phe	Glu	Gly	20	25	30	
Asp	Thr	Val	Ser	Leu	Gln	Cys	Thr	Tyr	Arg	Glu	Glu	Leu	Arg	Asp	35	40	45	
His	Arg	Lys	Tyr	Trp	Cys	Arg	Lys	Gly	Gly	Ile	Leu	Phe	Ser	Arg	50	55	60	
Cys	Ser	Gly	Thr	Ile	Tyr	Ala	Glu	Glu	Glu	Gly	Gln	Glu	Thr	Met	65	70	75	
Lys	Gly	Arg	Val	Ser	Ile	Arg	Asp	Ser	Arg	Gln	Glu	Leu	Ser	Leu	80	85	90	
Ile	Val	Thr	Leu	Trp	Asn	Leu	Thr	Leu	Gln	Asp	Ala	Gly	Glu	Tyr	95	100	105	
Trp	Cys	Gly	Val	Glu	Lys	Arg	Gly	Pro	Asp	Glu	Ser	Leu	Leu	Ile	110	115	120	
Ser	Leu	Phe	Val	Phe	Pro	Gly	Pro	Cys	Cys	Pro	Pro	Ser	Pro	Ser	125	130	135	
Pro	Thr	Phe	Gln	Pro	Leu	Ala	Thr	Thr	Arg	Leu	Gln	Pro	Lys	Ala	140	145	150	
Lys	Ala	Gln	Gln	Thr	Gln	Pro	Pro	Gly	Leu	Thr	Ser	Pro	Gly	Leu	155	160	165	
Tyr	Pro	Ala	Ala	Thr	Thr	Ala	Lys	Gln	Gly	Lys	Thr	Gly	Ala	Glu	170	175	180	
Ala	Pro	Pro	Leu	Pro	Gly	Thr	Ser	Gln	Tyr	Gly	His	Glu	Arg	Thr	185	190	195	
Ser	Gln	Tyr	Thr	Gly	Thr	Ser	Pro	His	Pro	Ala	Thr	Ser	Pro	Pro				

200	205	210
Ala Gly Ser Ser Arg Pro Pro Met Gln Leu Asp Ser Thr Ser Ala 215	220	225
Glu Asp Thr Ser Pro Ala Leu Ser Ser Gly Ser Ser Lys Pro Arg 230	235	240
Val Ser Ile Pro Met Val Arg Ile Leu Ala Pro Val Leu Val Leu 245	250	255
Leu Ser Leu Leu Ser Ala Ala Gly Leu Ile Ala Phe Cys Ser His 260	265	270
Leu Leu Leu Trp Arg Lys Glu Ala Gln Gln Ala Thr Glu Thr Gln 275	280	285
Arg Asn Glu Lys Phe Trp Leu Ser Arg Leu Thr Ala Glu Glu Lys 290	295	300
Glu Ala Pro Ser Gln Ala Pro Glu Gly Asp Val Ile Ser Met Pro 305	310	315
Pro Leu His Thr Ser Glu Glu Glu Leu Gly Phe Ser Lys Phe Val 320	325	330
Ser Ala		

<210> 217
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 217
 ccctgcagtg cacctacagg gaag 24

<210> 218
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 218
 ctgtcttccc ctgcttggt gtgg 24

<210> 219
 <211> 47
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

His Asp Phe Gly Leu Asp Gly Tyr Arg Gly Tyr Ser Leu Ala Asp
 35 40 45
 Trp Val Cys Leu Ala Tyr Phe Thr Ser Gly Phe Asn Ala Ala Ala
 50 55 60
 Leu Asp Tyr Glu Ala Asp Gly Ser Thr Asn Asn Gly Ile Phe Gln
 65 70 75
 Ile Asn Ser Arg Arg Trp Cys Ser Asn Leu Thr Pro Asn Val Pro
 80 85 90
 Asn Val Cys Arg Met Tyr Cys Ser Asp Leu Leu Asn Pro Asn Leu
 95 100 105
 Lys Asp Thr Val Ile Cys Ala Met Lys Ile Thr Gln Glu Pro Gln
 110 115 120
 Gly Leu Gly Tyr Trp Glu Ala Trp Arg His His Cys Gln Gly Lys
 125 130 135
 Asp Leu Thr Glu Trp Val Asp Gly Cys Asp Phe
 140 145

<210> 222

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 222

gggatcatgt tggtggccct ggtc 24

<210> 223

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 223

gcaaggcaga cccagtcagc cag 23

<210> 224

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 224

ctgcctgcta ccctccaagt gaggccaagc tctacggtcg ttgtg 45

<210> 225

<211> 2049
<212> DNA
<213> Homo sapiens

<400> 225
agccgctgcc ccgggcccggg cgcgcgcggc ggcacccatga gtccccgctc 50
gtgctgcgt tgcgtgcgcc tctcgtctt cgcgctcttc tcagccgccc 100
cgagcaactg gctgtacctg gccaaactgt cgtcgggtggg gagcatctca 150
gaggaggaga cgtgcgagaa actcaagggc ctgatccaga ggcaggtgca 200
gatgtgcaag cggaacctgg aagtcattga ctccgtgcgc cgcggtgcc 250
agctggccat tgaggagtgc cagtaccagt tccggaaccg gcgctggaac 300
tgctccacac tcgactcctt gcccgctctt ggcaagggtg tgacgcaagg 350
gactcgggag gcggccttcg tgtacgcat ctcttcggca ggtgtggcct 400
ttgcagtgc gcgggctgc agcagtggg agctggagaa gtgcggctgt 450
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ctctgacaac atgcctacg gtgtggcctt ctccagtcg tttgtggatg 550
tgccggagag aagcaagggg gcctcgtcca gcagagccct catgaacctc 600
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atgcaagtgc cacggggtgt caggctcctg tgaggtaaag acgtgctggc 700
gagccgtgcc gcccttcgc cagggtgggt acgcactgaa ggagaagttt 750
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ggtaccacgc aacgcacagt tcaagccga cacagatgag gacctggtgt 850
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ctggttttgt ttttgggtcc tcatgttatt tattgccga accaggcagg 1250
caacccaag ggcaccaacc agggcctccc caaagcctgg gcctttgtgg 1300
ctgccactga ccaaaggac ctgtcgtgc cgcgtggctg cccgcatgtg 1350

Ala	Phe	Ala	Val	Thr	Arg	Ala	Cys	Ser	Ser	Gly	Glu	Leu	Glu	Lys
				125					130					135
Cys	Gly	Cys	Asp	Arg	Thr	Val	His	Gly	Val	Ser	Pro	Gln	Gly	Phe
				140					145					150
Gln	Trp	Ser	Gly	Cys	Ser	Asp	Asn	Ile	Ala	Tyr	Gly	Val	Ala	Phe
				155					160					165
Ser	Gln	Ser	Phe	Val	Asp	Val	Arg	Glu	Arg	Ser	Lys	Gly	Ala	Ser
				170					175					180
Ser	Ser	Arg	Ala	Leu	Met	Asn	Leu	His	Asn	Asn	Glu	Ala	Gly	Arg
				185					190					195
Lys	Ala	Ile	Leu	Thr	His	Met	Arg	Val	Glu	Cys	Lys	Cys	His	Gly
				200					205					210
Val	Ser	Gly	Ser	Cys	Glu	Val	Lys	Thr	Cys	Trp	Arg	Ala	Val	Pro
				215					220					225
Pro	Phe	Arg	Gln	Val	Gly	His	Ala	Leu	Lys	Glu	Lys	Phe	Asp	Gly
				230					235					240
Ala	Thr	Glu	Val	Glu	Pro	Arg	Arg	Val	Gly	Ser	Ser	Arg	Ala	Leu
				245					250					255
Val	Pro	Arg	Asn	Ala	Gln	Phe	Lys	Pro	His	Thr	Asp	Glu	Asp	Leu
				260					265					270
Val	Tyr	Leu	Glu	Pro	Ser	Pro	Asp	Phe	Cys	Glu	Gln	Asp	Met	Arg
				275					280					285
Ser	Gly	Val	Leu	Gly	Thr	Arg	Gly	Arg	Thr	Cys	Asn	Lys	Thr	Ser
				290					295					300
Lys	Ala	Ile	Asp	Gly	Cys	Glu	Leu	Leu	Cys	Cys	Gly	Arg	Gly	Phe
				305					310					315
His	Thr	Ala	Gln	Val	Glu	Leu	Ala	Glu	Arg	Cys	Ser	Cys	Lys	Phe
				320					325					330
His	Trp	Cys	Cys	Phe	Val	Lys	Cys	Arg	Gln	Cys	Gln	Arg	Leu	Val
				335					340					345
Glu	Leu	His	Thr	Cys	Arg									
				350										

<210> 227

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 227

gctgcagctg caaattccac tgg 23

<210> 228
 <211> 28
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide probe

<400> 228
 tgggtgggaga ctgttttaa at tatcggcc 28

<210> 229
 <211> 41
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 229
 tgcttcgtca agtgccggca gtgccagcgg ctctgtggagt t 41

<210> 230
 <211> 1355
 <212> DNA
 <213> Homo sapiens

<400> 230
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 ggggtgcctgc atcgccatgg acaccaccag gtacagcaag tggggcgga 100
 gctccgagga ggtccccgga gggccctggg gacgctgggt gcaactggagc 150
 aggagacccc tcttcttggc cctggctgtc ctggtcacca cagtcctttg 200
 ggctgtgatt ctgagtatcc tattgtccaa ggccctccacg gagcgcgcg 250
 cgctgcttga cggccacgac ctgctgagga caaacgcctc gaagcagacg 300
 gcggcgctgg gtgcctgaa ggaggaggtc ggagactgcc acagctgctg 350
 ctcggggacg caggcgacg tgcagaccac gcgcgcggag cttggggagg 400
 cgcaggcgaa gctgatggag caggagagcg ccctgcggga actgcgtgag 450
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 gcgagccgtg cccacgctg tggctgtcct tcgagggtc ctgctacttt 600
 ttctctgtgc caaagacgac gtgggcggcg gcgcaggatc actgcgcaga 650
 tgccagcgcg cacctggtga tcgttggggg cctggatgag cagggttcc 700
 tcaactcgaa cacgcgtggc cgtggttact ggctgggcct gagggctgtg 750

cgccatctgg gcaaggttca gggctaccag tgggtggacg gagtctctct 800
cagcttcagc cactggaacc aggagagcc caatgacgct tgggggcgcg 850
agaactgtgt catgatgctg cacacggggc tgtggaacga cgcaccgtgt 900
gacagcgaga aggacggctg gatctgtgag aaaaggcaca actgctgacc 950
ccgcccagtg ccctggagcc gcgcccattg cagcatgtcg taccctgggg 1000
gtggttcacc tccctggctc ctggagctga ttgccaaaga gtttttttct 1050
tcctcatcca ccgctgctga gtctcagaaa cacttggccc aacatagccc 1100
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aaaaa 1355

<210> 231
<211> 293
<212> PRT
<213> Homo sapiens

<400> 231
Met Asp Thr Thr Arg Tyr Ser Lys Trp Gly Gly Ser Ser Glu Glu
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Val Pro Gly Gly Pro Trp Gly Arg Trp Val His Trp Ser Arg Arg
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Pro Leu Phe Leu Ala Leu Ala Val Leu Val Thr Thr Val Leu Trp
35 40 45
Ala Val Ile Leu Ser Ile Leu Leu Ser Lys Ala Ser Thr Glu Arg
50 55 60
Ala Ala Leu Leu Asp Gly His Asp Leu Leu Arg Thr Asn Ala Ser
65 70 75
Lys Gln Thr Ala Ala Leu Gly Ala Leu Lys Glu Glu Val Gly Asp
80 85 90
Cys His Ser Cys Cys Ser Gly Thr Gln Ala Gln Leu Gln Thr Thr
95 100 105
Arg Ala Glu Leu Gly Glu Ala Gln Ala Lys Leu Met Glu Gln Glu
110 115 120
Ser Ala Leu Arg Glu Leu Arg Glu Arg Val Thr Gln Gly Leu Ala
125 130 135

Glu	Ala	Gly	Arg	Gly	Arg	Glu	Asp	Val	Arg	Thr	Glu	Leu	Phe	Arg	
				140					145					150	
Ala	Leu	Glu	Ala	Val	Arg	Leu	Gln	Asn	Asn	Ser	Cys	Glu	Pro	Cys	
				155					160					165	
Pro	Thr	Ser	Trp	Leu	Ser	Phe	Glu	Gly	Ser	Cys	Tyr	Phe	Phe	Ser	
				170					175					180	
Val	Pro	Lys	Thr	Thr	Trp	Ala	Ala	Ala	Gln	Asp	His	Cys	Ala	Asp	
				185					190					195	
Ala	Ser	Ala	His	Leu	Val	Ile	Val	Gly	Gly	Leu	Asp	Glu	Gln	Gly	
				200					205					210	
Phe	Leu	Thr	Arg	Asn	Thr	Arg	Gly	Arg	Gly	Tyr	Trp	Leu	Gly	Leu	
				215					220					225	
Arg	Ala	Val	Arg	His	Leu	Gly	Lys	Val	Gln	Gly	Tyr	Gln	Trp	Val	
				230					235					240	
Asp	Gly	Val	Ser	Leu	Ser	Phe	Ser	His	Trp	Asn	Gln	Gly	Glu	Pro	
				245					250					255	
Asn	Asp	Ala	Trp	Gly	Arg	Glu	Asn	Cys	Val	Met	Met	Leu	His	Thr	
				260					265					270	
Gly	Leu	Trp	Asn	Asp	Ala	Pro	Cys	Asp	Ser	Glu	Lys	Asp	Gly	Trp	
				275					280					285	
Ile	Cys	Glu	Lys	Arg	His	Asn	Cys								
				290											

- <210> 232
- <211> 24
- <212> DNA
- <213> Artificial Sequence
- <220>
- <223> Synthetic oligonucleotide probe
- <400> 232
- gcgagaactg tgtcatgatg ctgc 24
- <210> 233
- <211> 24
- <212> DNA
- <213> Artificial Sequence
- <220>
- <223> Synthetic oligonucleotide probe
- <400> 233
- gtttctgaga ctcagcagcg gtgg 24
- <210> 234
- <211> 50
- <212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 234

caccgtgtga cagcgagaag gacggctgga tctgtgagaa aaggcacaac 50

<210> 235

<211> 1847

<212> DNA

<213> Homo sapiens

<400> 235

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ctccacgctc ctatctgcct ctcgctggag gccaggccgt gcagcatcga 150
agacaggagg aactggagcc tcattggccg gcccgggcg cggcctcgg 200
gcttaaataag gagctccggg ctctggctgg gacccgaccg ctgccggccg 250
cgctccccgt gctcctgcg ggtgatggaa aacccagcc cgccgcccgc 300
cctgggcaag gccctctgcg ctctcctcct ggccactctc ggccgcccgc 350
gccagcctct tgggggagag tccatctgtt ccgccagagc cccggccaaa 400
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cgcatagctc cgactacagc atgtggagga agaaccagta cgtcagtaac 550
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cagcgcaggc actcgtcgtt ctcgtttctg gtgcgcatcg tgcccagccc 750
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ggcgggaaca ggcggcgctg gacctgtacc cctacgacgc cgggacggac 850
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cggctgcgac agagccccag ggccttcac cctccgccc cagtctgccc 1050
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tggactgcga ggtctccctg tggtcgtcct ggggactgtg cggaggccac 1150
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 agcggggggc acttgagaag tgaataaatg gggcggtttc ggaagcgtca 1750
 gtgtttccat gttatggatc tctctgcgtt tgaataaaga ctatctctgt 1800
 tgctcacaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaa 1847

<210> 236

<211> 331

<212> PRT

<213> Homo sapiens

<400> 236

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				20					25					30
Gly	Glu	Ser	Ile	Cys	Ser	Ala	Arg	Ala	Pro	Ala	Lys	Tyr	Ser	Ile
				35					40					45
Thr	Phe	Thr	Gly	Lys	Trp	Ser	Gln	Thr	Ala	Phe	Pro	Lys	Gln	Tyr
				50					55					60
Pro	Leu	Phe	Arg	Pro	Pro	Ala	Gln	Trp	Ser	Ser	Leu	Leu	Gly	Ala
				65					70					75
Ala	His	Ser	Ser	Asp	Tyr	Ser	Met	Trp	Arg	Lys	Asn	Gln	Tyr	Val
				80					85					90
Ser	Asn	Gly	Leu	Arg	Asp	Phe	Ala	Glu	Arg	Gly	Glu	Ala	Trp	Ala
				95					100					105
Leu	Met	Lys	Glu	Ile	Glu	Ala	Ala	Gly	Glu	Ala	Leu	Gln	Ser	Val

	110		115		120
His Glu Val Phe	Ser Ala Pro Ala Val	Pro Ser Gly Thr Gly Gln			
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Thr Ser Ala Glu	Leu Glu Val Gln Arg	Arg His Ser Leu Val Ser			
	140	145			150
Phe Val Val Arg	Ile Val Pro Ser Pro	Asp Trp Phe Val Gly Val			
	155	160			165
Asp Ser Leu Asp	Leu Cys Asp Gly Asp	Arg Trp Arg Glu Gln Ala			
	170	175			180
Ala Leu Asp Leu	Tyr Pro Tyr Asp Ala	Gly Thr Asp Ser Gly Phe			
	185	190			195
Thr Phe Ser Ser	Pro Asn Phe Ala Thr	Ile Pro Gln Asp Thr Val			
	200	205			210
Thr Glu Ile Thr	Ser Ser Ser Pro Ser	His Pro Ala Asn Ser Phe			
	215	220			225
Tyr Tyr Pro Arg	Leu Lys Ala Leu Pro	Pro Ile Ala Arg Val Thr			
	230	235			240
Leu Leu Arg Leu	Arg Gln Ser Pro Arg	Ala Phe Ile Pro Pro Ala			
	245	250			255
Pro Val Leu Pro	Ser Arg Asp Asn Glu	Ile Val Asp Ser Ala Ser			
	260	265			270
Val Pro Glu Thr	Pro Leu Asp Cys Glu	Val Ser Leu Trp Ser Ser			
	275	280			285
Trp Gly Leu Cys	Gly Gly His Cys Gly	Arg Leu Gly Thr Lys Ser			
	290	295			300
Arg Thr Arg Tyr	Val Arg Val Gln Pro	Ala Asn Asn Gly Ser Pro			
	305	310			315
Cys Pro Glu Leu	Glu Glu Glu Ala Glu	Cys Val Pro Asp Asn Cys			
	320	325			330
Val					

<210> 237
 <211> 22
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 237
 cagcactgcc aggggaagag gg 22

<210> 238
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 238
caggactcgc tacgtccg 18

<210> 239
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 239
cagcccccttc tctctctttc tccc 24

<210> 240
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 240
gcagttatca gggacgcact cagcc 25

<210> 241
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 241
ccagcgagag gcagatag 18

<210> 242
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 242
cggtcaccgt gtcctgcggg atg 23

<210> 243
<211> 42
<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 243

cagcccccttc tcttcctttc tcccacgtcc tatctgcctc tc 42

<210> 244

<211> 1894

<212> DNA

<213> Homo sapiens

<400> 244

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tcatcccccg taaggagcag agtcctttgt actgaccaag atgagcaaca 200
tctacatcca ggagcctccc acgaatggga aggttttatt gaaaactaca 250
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gatgaactta acaataagca taccatotff ggaaaggffa caggggatac 600
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catgtgtttt ttcctagctg accttttata ttgctaaatc tgaaataaaa 1850
taactttcct tccacaaaaa aaaaaaaaaa aaaaaaaaaa aaaa 1894

<210> 245
<211> 472
<212> PRT
<213> Homo sapiens

<400> 245
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Leu Leu Lys Thr Thr Ala Gly Asp Ile Asp Ile Glu Leu Trp Ser
20 25 30
Lys Glu Ala Pro Lys Ala Cys Arg Asn Phe Ile Gln Leu Cys Leu
35 40 45
Glu Ala Tyr Tyr Asp Asn Thr Ile Phe His Arg Val Val Pro Gly
50 55 60
Phe Ile Val Gln Gly Gly Asp Pro Thr Gly Thr Gly Ser Gly Gly
65 70 75
Glu Ser Ile Tyr Gly Ala Pro Phe Lys Asp Glu Phe His Ser Arg
80 85 90
Leu Arg Phe Asn Arg Arg Gly Leu Val Ala Met Ala Asn Ala Gly
95 100 105

Ser His Asp Asn Gly Ser Gln Phe Phe Phe Thr Leu Gly Arg Ala	110	115	120
Asp Glu Leu Asn Asn Lys His Thr Ile Phe Gly Lys Val Thr Gly	125	130	135
Asp Thr Val Tyr Asn Met Leu Arg Leu Ser Glu Val Asp Ile Asp	140	145	150
Asp Asp Glu Arg Pro His Asn Pro His Lys Ile Lys Ser Cys Glu	155	160	165
Val Leu Phe Asn Pro Phe Asp Asp Ile Ile Pro Arg Glu Ile Lys	170	175	180
Arg Leu Lys Lys Glu Lys Pro Glu Glu Glu Val Lys Lys Leu Lys	185	190	195
Pro Lys Gly Thr Lys Asn Phe Ser Leu Leu Ser Phe Gly Glu Glu	200	205	210
Ala Glu Glu Glu Glu Glu Glu Val Asn Arg Val Ser Gln Ser Met	215	220	225
Lys Gly Lys Ser Lys Ser Ser His Asp Leu Leu Lys Asp Asp Pro	230	235	240
His Leu Ser Ser Val Pro Val Val Glu Ser Glu Lys Gly Asp Ala	245	250	255
Pro Asp Leu Val Asp Asp Gly Glu Asp Glu Ser Ala Glu His Asp	260	265	270
Glu Tyr Ile Asp Gly Asp Glu Lys Asn Leu Met Arg Glu Arg Ile	275	280	285
Ala Lys Lys Leu Lys Lys Asp Thr Ser Ala Asn Val Lys Ser Ala	290	295	300
Gly Glu Gly Glu Val Glu Lys Lys Ser Val Ser Arg Ser Glu Glu	305	310	315
Leu Arg Lys Glu Ala Arg Gln Leu Lys Arg Glu Leu Leu Ala Ala	320	325	330
Lys Gln Lys Lys Val Glu Asn Ala Ala Lys Gln Ala Glu Lys Arg	335	340	345
Ser Glu Glu Glu Glu Ala Pro Pro Asp Gly Ala Val Ala Glu Tyr	350	355	360
Arg Arg Glu Lys Gln Lys Tyr Glu Ala Leu Arg Lys Gln Gln Ser	365	370	375
Lys Lys Gly Thr Ser Arg Glu Asp Gln Thr Leu Ala Leu Leu Asn	380	385	390
Gln Phe Lys Ser Lys Leu Thr Gln Ala Ile Ala Glu Thr Pro Glu			

395	400	405
Asn Asp Ile Pro Glu Thr Glu Val Glu Asp Asp Glu Gly Trp Met		
410	415	420
Ser His Val Leu Gln Phe Glu Asp Lys Ser Arg Lys Val Lys Asp		
425	430	435
Ala Ser Met Gln Asp Ser Asp Thr Phe Glu Ile Tyr Asp Pro Arg		
440	445	450
Asn Pro Val Asn Lys Arg Arg Arg Glu Glu Ser Lys Lys Leu Met		
455	460	465
Arg Glu Lys Lys Glu Arg Arg		
470		

<210> 246

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 246

tgcgagatc ctactggcac aggg 24

<210> 247

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 247

cgagttagtc agagcatg 18

<210> 248

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 248

cagatggtgc tggtgccg 18

<210> 249

<211> 29

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

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<400> 249
  caactggaac aggaactgag atgtggatc 29

<210> 250
<211> 24
<212> DNA
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<220>
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<400> 250
  ctggttcagc agtgcaaggg tctg 24

<210> 251
<211> 18
<212> DNA
<213> Artificial Sequence

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<223> Synthetic oligonucleotide probe

<400> 251
  cctctccgat taaaacgc 18

<210> 252
<211> 45
<212> DNA
<213> Artificial Sequence

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<223> Synthetic oligonucleotide probe

<400> 252
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<210> 253
<211> 2456
<212> DNA
<213> Homo sapiens

<400> 253
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  catttcgcct tgctgacggc gtcgagccct ggccagacat gtccacaggg 150
  ttctccttcg ggtccgggac tctgggctcc accaccgtgg ccgcccggcg 200
  gaccagcaca ggcggcggttt tctccttcgg aacgggaacg tctagcaacc 250
  cttctgtggg gctcaatttt ggaaatcttg gaagtacttc aactccagca 300
  actacatctg ctctttcaag tggttttgga accgggctct ttggatctaa 350
  acctgccact gggttcactc taggaggaac aaatacaggt gccttgca 400

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ccaagaggcc tcaagtggtc accaaatatg gaaccctgca aggaaaacag 450
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cagacctoct ctaggtatcc tcaggtttgc acctccagaa cccccggagc 550
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gctctgtcgc caggctggag tgcagtggca cgatctcggc tcaactgcaac 650
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Pro	Glu	Pro	Trp	Lys	Gly	Ile	Arg	Asp	Ala	Thr	Thr	Tyr	Pro	Pro	
				140					145					150	
Gly	Trp	Ser	Leu	Ala	Leu	Ser	Pro	Gly	Trp	Ser	Ala	Val	Ala	Arg	
				155					160					165	
Ser	Arg	Leu	Thr	Ala	Thr	Ser	Ala	Ser	Arg	Val	Gln	Ala	Ser	Leu	
				170					175					180	
Leu	Pro	Gln	Pro	Leu	Ser	Val	Trp	Gly	Tyr	Arg	Cys	Leu	Gln	Glu	
				185					190					195	
Ser	Trp	Gly	Gln	Leu	Ala	Ser	Met	Tyr	Val	Ser	Thr	Arg	Glu	Arg	
				200					205					210	
Tyr	Lys	Trp	Leu	Arg	Phe	Ser	Glu	Asp	Cys	Leu	Tyr	Leu	Asn	Val	
				215					220					225	
Tyr	Ala	Pro	Ala	Arg	Ala	Pro	Gly	Asp	Pro	Gln	Leu	Pro	Val	Met	
				230					235					240	
Val	Trp	Phe	Pro	Gly	Gly	Ala	Phe	Ile	Val	Gly	Ala	Ala	Ser	Ser	
				245					250					255	
Tyr	Glu	Gly	Ser	Asp	Leu	Ala	Ala	Arg	Glu	Lys	Val	Val	Leu	Val	
				260					265					270	
Phe	Leu	Gln	His	Arg	Leu	Gly	Ile	Phe	Gly	Phe	Leu	Ser	Thr	Asp	
				275					280					285	
Asp	Ser	His	Ala	Arg	Gly	Asn	Trp	Gly	Leu	Leu	Asp	Gln	Met	Ala	
				290					295					300	
Ala	Leu	Arg	Trp	Val	Gln	Glu	Asn	Ile	Ala	Ala	Phe	Gly	Gly	Asp	
				305					310					315	
Pro	Gly	Asn	Val	Thr	Leu	Phe	Gly	Gln	Ser	Ala	Gly	Ala	Met	Ser	
				320					325					330	
Ile	Ser	Gly	Leu	Met	Met	Ser	Pro	Leu	Ala	Ser	Gly	Leu	Phe	His	
				335					340					345	
Arg	Ala	Ile	Ser	Gln	Ser	Gly	Thr	Ala	Leu	Phe	Arg	Leu	Phe	Ile	
				350					355					360	
Thr	Ser	Asn	Pro	Leu	Lys	Val	Ala	Lys	Lys	Val	Ala	His	Leu	Ala	
				365					370					375	
Gly	Cys	Asn	His	Asn	Ser	Thr	Gln	Ile	Leu	Val	Asn	Cys	Leu	Arg	
				380					385					390	
Ala	Leu	Ser	Gly	Thr	Lys	Val	Met	Arg	Val	Ser	Asn	Lys	Met	Arg	
				395					400					405	
Phe	Leu	Gln	Leu	Asn	Phe	Gln	Arg	Asp	Pro	Glu	Glu	Ile	Ile	Trp	
				410					415					420	
Ser	Met	Ser	Pro	Val	Val	Asp	Gly	Val	Val	Ile	Pro	Asp	Asp	Pro	

425	430	435
Leu Val Leu Leu Thr Gln Gly Lys Val	Ser Ser Val Pro Tyr Leu	
440	445	450
Leu Gly Val Asn Asn Leu Glu Phe Asn	Trp Leu Leu Pro Tyr Asn	
455	460	465
Ile Thr Lys Glu Gln Val Pro Leu Val	Val Glu Glu Tyr Leu Asp	
470	475	480
Asn Val Asn Glu His Asp Trp Lys Met	Leu Arg Asn Arg Met Met	
485	490	495
Asp Ile Val Gln Asp Ala Thr Phe Val	Tyr Ala Thr Leu Gln Thr	
500	505	510
Ala His Tyr His Arg Glu Thr Pro Met	Met Gly Ile Cys Pro Ala	
515	520	525
Gly His Ala Thr Thr Arg Met Lys Ser	Thr Cys Ser Trp Ile Leu	
530	535	540
Pro Gln Glu Trp Ala		
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 <211> 23
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 255
 aggtgcctgc aggagtctg ggg 23

<210> 256
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 256
 ccacctcagg aagccgaaga tgcc 24

<210> 257
 <211> 45
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 257
 gaacggtaca agtggctgcg cttcagcgag gactgtctgt acctg 45

<210> 258
 <211> 2764
 <212> DNA
 <213> Homo sapiens

<400> 258
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 actgccactg ctgctgtcct cgctgctggg cgggtcccag gctatggatg 100
 ggagattctg gatacgagtg caggagtcag tgatggtgcc ggagggcctg 150
 tgcattctctg tgccctgctc tttctcctac ccccgacaag actggacagg 200
 gtctacccca gcttatggct actggttcaa agcagtgact gagacaacca 250
 aggggtgctcc tgtggccaca aaccaccaga gtcgagaggt ggaaatgagc 300
 acccgggggc gattccagct cactggggat cccgccaagg ggaactgctc 350
 cttggtgatc agagacgcgc agatgcagga tgagtcacag tacttctttc 400
 ggggtggagag aggaagctat gtgacatata atttcatgaa cgatggggttc 450
 tttctaaaag taacagtgtc cagcttcacg cccagacccc aggaccacaa 500
 caccgacctc acctgccatg tggacttctc cagaaagggg gtgagcgcac 550
 agaggaccgt ccgactccgt gtggcctatg cccccagaga ccttggtatc 600
 agcatttcac gtgacaacac gccagccctg gagccccagc cccagggaaa 650
 tgtcccatc ctggaagccc aaaaaggcca gttcctgcgg ctccctctgtg 700
 ctgctgacag ccagccccct gccacactga gctgggtcct gcagaacaga 750
 gtccctctct cgtcccatcc ctggggccct agaccctgg ggctggagct 800
 gcccggggtg aaggctgggg attcagggcg ctacacctgc cgagcggaga 850
 acaggcttgg ctcccagcag cgagccctgg acctctctgt gcagtatcct 900
 ccagagaacc tgagagtgat ggtttcccaa gcaaacagga cagtccctgga 950
 aaaccttggg aacggcacgt ctctcccagt actggagggc caaagcctgt 1000
 gcctgggtctg tgtcacacac agcagcccc cagccaggct gagctggacc 1050
 cagaggggac aggtttctgag cccctccag cctcagacc ccggggtcct 1100
 ggagctgcct cgggttcaag tggagcacga aggagagttc acctgccacg 1150
 ctcggcaccc actgggtctc cagcacgtct ctctcagcct ctccgtgcac 1200
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 aatcggcac acggtctctc ttttctctg cctggccctg atcatcatga 1300

agattctacc gaagagacgg actcagacag aaaccccgag gccaggttc 1350
 tcccggcaca gcacgatcct ggattacatc aatgtggtcc cgacggctgg 1400
 ccccttggtc cagaagcggc atcagaaaagc cacaccaaac agtcctcgga 1450
 cccctcctcc accaggtgct ccctccccag aatcaaagaa gaaccagaaa 1500
 aagcagtatc agttgcccag tttcccagaa cccaaatcat ccactcaagc 1550
 cccagaatcc caggagagcc aagaggagct ccattatgcc acgctcaact 1600
 tcccaggcgt cagaccagc cctgaggccc ggatgcccaa gggcaccag 1650
 gcggattatg cagaagtcaa gttccaatga gggctcttta ggcttttagga 1700
 ctgggacttc ggctagggag gaaggtagag taagaggttg aagataacag 1750
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 gcctgtaatc ccagcacttt gggaggttga ggtgggcaga tcgcctgagg 1900
 tcgggagttc gagaccagcc tggccaactt ggtgaaaccc cgtctctact 1950
 aaaaatacaa aaattagctg ggcatggttg caggcgctg taatcctacc 2000
 tacttgggaa gctgaggcag gagaatcact tgaacctggg agacggaggt 2050
 tgcagtgagc caagatcaca ccattgcacg ccagcctggg caacaaagcg 2100
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 cccagcactt tgggaggcta aggtgggttg attgcttgag cccaggagtt 2200
 cgagaccagc ctgggcaaca tggtgaaacc ccattctctac aaaaaataca 2250
 aaacatagct gggcttggtg gtgtgtgcct gtagtcccag ctgtcagaca 2300
 tttaaaccag agcaactcca tctggaatag gagctgaata aaatgaggct 2350
 gagacctact gggctgcatt ctgagacagt ggaggcattc taagtcacag 2400
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 gccacgagag tgacctctgg tcgtcctcac tgctacactc ctgacagcac 2550
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 cccaaaaggg ggaggaatga ataatccacc ccttgtttag caaataagca 2650
 agaaataacc ataaaagtgg gcaaccagca gctctaggcg ctgctcttgt 2700
 ctatggagta gccattcttt tgttccttta cttctttaat aaacttgctt 2750

tcaccttaaa aaaa 2764

<210> 259

<211> 544

<212> PRT

<213> Homo sapiens

<400> 259

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Ala	Met	Asp	Gly	Arg	Phe	Trp	Ile	Arg	Val	Gln	Glu	Ser	Val	Met
				20					25					30
Val	Pro	Glu	Gly	Leu	Cys	Ile	Ser	Val	Pro	Cys	Ser	Phe	Ser	Tyr
				35					40					45
Pro	Arg	Gln	Asp	Trp	Thr	Gly	Ser	Thr	Pro	Ala	Tyr	Gly	Tyr	Trp
				50					55					60
Phe	Lys	Ala	Val	Thr	Glu	Thr	Thr	Lys	Gly	Ala	Pro	Val	Ala	Thr
				65					70					75
Asn	His	Gln	Ser	Arg	Glu	Val	Glu	Met	Ser	Thr	Arg	Gly	Arg	Phe
				80					85					90
Gln	Leu	Thr	Gly	Asp	Pro	Ala	Lys	Gly	Asn	Cys	Ser	Leu	Val	Ile
				95					100					105
Arg	Asp	Ala	Gln	Met	Gln	Asp	Glu	Ser	Gln	Tyr	Phe	Phe	Arg	Val
				110					115					120
Glu	Arg	Gly	Ser	Tyr	Val	Thr	Tyr	Asn	Phe	Met	Asn	Asp	Gly	Phe
				125					130					135
Phe	Leu	Lys	Val	Thr	Val	Leu	Ser	Phe	Thr	Pro	Arg	Pro	Gln	Asp
				140					145					150
His	Asn	Thr	Asp	Leu	Thr	Cys	His	Val	Asp	Phe	Ser	Arg	Lys	Gly
				155					160					165
Val	Ser	Ala	Gln	Arg	Thr	Val	Arg	Leu	Arg	Val	Ala	Tyr	Ala	Pro
				170					175					180
Arg	Asp	Leu	Val	Ile	Ser	Ile	Ser	Arg	Asp	Asn	Thr	Pro	Ala	Leu
				185					190					195
Glu	Pro	Gln	Pro	Gln	Gly	Asn	Val	Pro	Tyr	Leu	Glu	Ala	Gln	Lys
				200					205					210
Gly	Gln	Phe	Leu	Arg	Leu	Leu	Cys	Ala	Ala	Asp	Ser	Gln	Pro	Pro
				215					220					225
Ala	Thr	Leu	Ser	Trp	Val	Leu	Gln	Asn	Arg	Val	Leu	Ser	Ser	Ser
				230					235					240
His	Pro	Trp	Gly	Pro	Arg	Pro	Leu	Gly	Leu	Glu	Leu	Pro	Gly	Val
				245					250					255

Lys	Ala	Gly	Asp	Ser	Gly	Arg	Tyr	Thr	Cys	Arg	Ala	Glu	Asn	Arg	
				260					265					270	
Leu	Gly	Ser	Gln	Gln	Arg	Ala	Leu	Asp	Leu	Ser	Val	Gln	Tyr	Pro	
				275					280					285	
Pro	Glu	Asn	Leu	Arg	Val	Met	Val	Ser	Gln	Ala	Asn	Arg	Thr	Val	
				290					295					300	
Leu	Glu	Asn	Leu	Gly	Asn	Gly	Thr	Ser	Leu	Pro	Val	Leu	Glu	Gly	
				305					310					315	
Gln	Ser	Leu	Cys	Leu	Val	Cys	Val	Thr	His	Ser	Ser	Pro	Pro	Ala	
				320					325					330	
Arg	Leu	Ser	Trp	Thr	Gln	Arg	Gly	Gln	Val	Leu	Ser	Pro	Ser	Gln	
				335					340					345	
Pro	Ser	Asp	Pro	Gly	Val	Leu	Glu	Leu	Pro	Arg	Val	Gln	Val	Glu	
				350					355					360	
His	Glu	Gly	Glu	Phe	Thr	Cys	His	Ala	Arg	His	Pro	Leu	Gly	Ser	
				365					370					375	
Gln	His	Val	Ser	Leu	Ser	Leu	Ser	Val	His	Tyr	Lys	Lys	Gly	Leu	
				380					385					390	
Ile	Ser	Thr	Ala	Phe	Ser	Asn	Gly	Ala	Phe	Leu	Gly	Ile	Gly	Ile	
				395					400					405	
Thr	Ala	Leu	Leu	Phe	Leu	Cys	Leu	Ala	Leu	Ile	Ile	Met	Lys	Ile	
				410					415					420	
Leu	Pro	Lys	Arg	Arg	Thr	Gln	Thr	Glu	Thr	Pro	Arg	Pro	Arg	Phe	
				425					430					435	
Ser	Arg	His	Ser	Thr	Ile	Leu	Asp	Tyr	Ile	Asn	Val	Val	Pro	Thr	
				440					445					450	
Ala	Gly	Pro	Leu	Ala	Gln	Lys	Arg	Asn	Gln	Lys	Ala	Thr	Pro	Asn	
				455					460					465	
Ser	Pro	Arg	Thr	Pro	Pro	Pro	Pro	Gly	Ala	Pro	Ser	Pro	Glu	Ser	
				470					475					480	
Lys	Lys	Asn	Gln	Lys	Lys	Gln	Tyr	Gln	Leu	Pro	Ser	Phe	Pro	Glu	
				485					490					495	
Pro	Lys	Ser	Ser	Thr	Gln	Ala	Pro	Glu	Ser	Gln	Glu	Ser	Gln	Glu	
				500					505					510	
Glu	Leu	His	Tyr	Ala	Thr	Leu	Asn	Phe	Pro	Gly	Val	Arg	Pro	Arg	
				515					520					525	
Pro	Glu	Ala	Arg	Met	Pro	Lys	Gly	Thr	Gln	Ala	Asp	Tyr	Ala	Glu	
				530					535					540	
Val	Lys	Phe	Gln												

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<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 260
caaagcctgc gcctggtctg tg 22

<210> 261
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 261
ttctggagcc cagaggtgc tgag 24

<210> 262
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 262
ggagctgcca cccattcaaa tggagcacga aggagagttc acctg 45

<210> 263
<211> 2857
<212> DNA
<213> Homo sapiens

<400> 263
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actgctgcgt tttatgttgg gaattcctct cctatggcct tgtcttggag 100
caacagaaaa ctctcaaaaca aagaaagtca agcagccagt gcgatctcat 150
ttgagagtga agcgtggctg ggtgtggaac caattttttg taccagagga 200
aatgaatacg actagtcatc acatcggcca gctaagatct gatttagaca 250
atggaaacaa ttctttccag tacaagcttt tgggagctgg agctggaagt 300
acttttatca ttgatgaaag aacaggtgac atatatgcca tacagaagct 350
tgatagagag gagcgatccc tctacatctt aagagcccag gtaatagaca 400
tcgctactgg aagggtgtg gaacctgagt ctgagtttgt catcaaagtt 450

tcggatatca atgacaatga accaaaattc ctagatgaac cttatgaggc 500
cattgtacca gagatgtctc cagaaggaac attagttatc caggtgacag 550
caagtgatgc tgacgatccc tcaagtggta ataatgctcg tctcctctac 600
agcttacttc aaggccagcc atatttttct gttgaaccaa caacaggagt 650
cataagaata tcttctaaaa tggatagaga actgcaagat gagtattggg 700
taatcattca agccaaggac atgattggtc agccaggagc gttgtctgga 750
acaacaagtg tattaattaa actttcagat gttaatgaca ataagcctat 800
atttaaagaa agtttatacc gcttgactgt ctctgaatct gcacccactg 850
ggacttctat aggaacaatc atggcatatg ataatgacat aggagagaat 900
gcagaaatgg attacagcat tgaagaggat gattcgcaaa cttttgacat 950
tattactaat catgaaactc aagaaggaat agttatatta aaaaagaaag 1000
tggattttga gcaccagaac cactacggta ttagagcaaa agttaaaaac 1050
catcatgttc ctgagcagct catgaagtac cacactgagg cttccaccac 1100
tttcattaag atccagggtg aagatgttga tgagcctcct cttttcctcc 1150
ttccatatta tgtatttgaa gtttttgaag aaaccccaca gggatcattt 1200
gtaggcgtgg tgtctgccac agaccagac aataggaaat ctcctatcag 1250
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tcactacaag taactcactg gatcgtgaaa tcagtgcttg gtacaaccta 1350
agtattacag ccacagaaaa atacaatata gaacagatct cttcgatccc 1400
actgtatgtg caagttctta acatcaatga tcatgctcct gagttctctc 1450
aatactatga gacttatgtt tgtgaaaatg caggtctctg tcaggtaatt 1500
cagactatca gtgcagtga tagagatgaa tccatagaag agcaccattt 1550
ttactttaat ctatctgtag aagacactaa caattcaagt tttacaatca 1600
tagataatca agataacaca gctgtcattt tgactaatag aactggtttt 1650
aaccttcaag aagaacctgt cttctacatc tccatcttaa ttgccgacaa 1700
tggaatcccg tcacttacia gtacaaacac cottaccatc catgtctgtg 1750
actgtggtga cagtgggagc acacagacct gccagtacca ggagcttgtg 1800
ctttccatgg gattcaagac agaagttatc attgctatc tcatttgcac 1850
tatgatcata tttgggttta tttttttgac tttgggttta aaacaacgga 1900

His	His	Ile	Gly	Gln	Leu	Arg	Ser	Asp	Leu	Asp	Asn	Gly	Asn	Asn			
				65					70					75			
Ser	Phe	Gln	Tyr	Lys	Leu	Leu	Gly	Ala	Gly	Ala	Gly	Ser	Thr	Phe			
				80					85					90			
Ile	Ile	Asp	Glu	Arg	Thr	Gly	Asp	Ile	Tyr	Ala	Ile	Gln	Lys	Leu			
				95					100					105			
Asp	Arg	Glu	Glu	Arg	Ser	Leu	Tyr	Ile	Leu	Arg	Ala	Gln	Val	Ile			
				110					115					120			
Asp	Ile	Ala	Thr	Gly	Arg	Ala	Val	Glu	Pro	Glu	Ser	Glu	Phe	Val			
				125					130					135			
Ile	Lys	Val	Ser	Asp	Ile	Asn	Asp	Asn	Glu	Pro	Lys	Phe	Leu	Asp			
				140					145					150			
Glu	Pro	Tyr	Glu	Ala	Ile	Val	Pro	Glu	Met	Ser	Pro	Glu	Gly	Thr			
				155					160					165			
Leu	Val	Ile	Gln	Val	Thr	Ala	Ser	Asp	Ala	Asp	Asp	Pro	Ser	Ser			
				170					175					180			
Gly	Asn	Asn	Ala	Arg	Leu	Leu	Tyr	Ser	Leu	Leu	Gln	Gly	Gln	Pro			
				185					190					195			
Tyr	Phe	Ser	Val	Glu	Pro	Thr	Thr	Gly	Val	Ile	Arg	Ile	Ser	Ser			
				200					205					210			
Lys	Met	Asp	Arg	Glu	Leu	Gln	Asp	Glu	Tyr	Trp	Val	Ile	Ile	Gln			
				215					220					225			
Ala	Lys	Asp	Met	Ile	Gly	Gln	Pro	Gly	Ala	Leu	Ser	Gly	Thr	Thr			
				230					235					240			
Ser	Val	Leu	Ile	Lys	Leu	Ser	Asp	Val	Asn	Asp	Asn	Lys	Pro	Ile			
				245					250					255			
Phe	Lys	Glu	Ser	Leu	Tyr	Arg	Leu	Thr	Val	Ser	Glu	Ser	Ala	Pro			
				260					265					270			
Thr	Gly	Thr	Ser	Ile	Gly	Thr	Ile	Met	Ala	Tyr	Asp	Asn	Asp	Ile			
				275					280					285			
Gly	Glu	Asn	Ala	Glu	Met	Asp	Tyr	Ser	Ile	Glu	Glu	Asp	Asp	Ser			
				290					295					300			
Gln	Thr	Phe	Asp	Ile	Ile	Thr	Asn	His	Glu	Thr	Gln	Glu	Gly	Ile			
				305					310					315			
Val	Ile	Leu	Lys	Lys	Lys	Val	Asp	Phe	Glu	His	Gln	Asn	His	Tyr			
				320					325					330			
Gly	Ile	Arg	Ala	Lys	Val	Lys	Asn	His	His	Val	Pro	Glu	Gln	Leu			
				335					340					345			
Met	Lys	Tyr	His	Thr	Glu	Ala	Ser	Thr	Thr	Phe	Ile	Lys	Ile	Gln			

	350		355		360
Val Glu Asp Val	Asp Glu Pro Pro Leu	Phe Leu Leu Pro Tyr Tyr			
	365	370			375
Val Phe Glu Val	Phe Glu Glu Thr Pro	Gln Gly Ser Phe Val Gly			
	380	385			390
Val Val Ser Ala	Thr Asp Pro Asp Asn	Arg Lys Ser Pro Ile Arg			
	395	400			405
Tyr Ser Ile Thr	Arg Ser Lys Val Phe	Asn Ile Asn Asp Asn Gly			
	410	415			420
Thr Ile Thr Thr	Ser Asn Ser Leu Asp	Arg Glu Ile Ser Ala Trp			
	425	430			435
Tyr Asn Leu Ser	Ile Thr Ala Thr Glu	Lys Tyr Asn Ile Glu Gln			
	440	445			450
Ile Ser Ser Ile	Pro Leu Tyr Val Gln	Val Leu Asn Ile Asn Asp			
	455	460			465
His Ala Pro Glu	Phe Ser Gln Tyr Tyr	Glu Thr Tyr Val Cys Glu			
	470	475			480
Asn Ala Gly Ser	Gly Gln Val Ile Gln	Thr Ile Ser Ala Val Asp			
	485	490			495
Arg Asp Glu Ser	Ile Glu Glu His His	Phe Tyr Phe Asn Leu Ser			
	500	505			510
Val Glu Asp Thr	Asn Asn Ser Ser Phe	Thr Ile Ile Asp Asn Gln			
	515	520			525
Asp Asn Thr Ala	Val Ile Leu Thr Asn	Arg Thr Gly Phe Asn Leu			
	530	535			540
Gln Glu Glu Pro	Val Phe Tyr Ile Ser	Ile Leu Ile Ala Asp Asn			
	545	550			555
Gly Ile Pro Ser	Leu Thr Ser Thr Asn	Thr Leu Thr Ile His Val			
	560	565			570
Cys Asp Cys Gly	Asp Ser Gly Ser Thr	Gln Thr Cys Gln Tyr Gln			
	575	580			585
Glu Leu Val Leu	Ser Met Gly Phe Lys	Thr Glu Val Ile Ile Ala			
	590	595			600
Ile Leu Ile Cys	Ile Met Ile Ile Phe	Gly Phe Ile Phe Leu Thr			
	605	610			615
Leu Gly Leu Lys	Gln Arg Arg Lys Gln	Ile Leu Phe Pro Glu Lys			
	620	625			630
Ser Glu Asp Phe	Arg Glu Asn Ile Phe	Gln Tyr Asp Asp Glu Gly			
	635	640			645

Gly	Gly	Glu	Glu	Asp	Thr	Glu	Ala	Phe	Asp	Ile	Ala	Glu	Leu	Arg
				650					655					660
Ser	Ser	Thr	Ile	Met	Arg	Glu	Arg	Lys	Thr	Arg	Lys	Thr	Thr	Ser
				665					670					675
Ala	Glu	Ile	Arg	Ser	Leu	Tyr	Arg	Gln	Ser	Leu	Gln	Val	Gly	Pro
				680					685					690
Asp	Ser	Ala	Ile	Phe	Arg	Lys	Phe	Ile	Leu	Glu	Lys	Leu	Glu	Glu
				695					700					705
Ala	Asn	Thr	Asp	Pro	Cys	Ala	Pro	Pro	Phe	Asp	Ser	Leu	Gln	Thr
				710					715					720
Tyr	Ala	Phe	Glu	Gly	Thr	Gly	Ser	Leu	Ala	Gly	Ser	Leu	Ser	Ser
				725					730					735
Leu	Glu	Ser	Ala	Val	Ser	Asp	Gln	Asp	Glu	Ser	Tyr	Asp	Tyr	Leu
				740					745					750
Asn	Glu	Leu	Gly	Pro	Arg	Phe	Lys	Arg	Leu	Ala	Cys	Met	Phe	Gly
				755					760					765
Ser	Ala	Val	Gln	Ser	Asn	Asn								
				770										

<210> 265
 <211> 349
 <212> DNA
 <213> Homo sapiens

<220>
 <221> unsure
 <222> 24, 60, 141, 226, 228, 249, 252
 <223> unknown base

<400> 265
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 gaatatatttn taaaatggat agagaactgc aagatgagta ttgggtaatc 100
 attcaagcca aggacatgat tggtcagcca ggagcgttgt ntggaacaac 150
 aagtgtatta attaaacttt cagatggtta tgacaataag cctatattta 200
 aagaaagttt ataccgcttg actgtntntg aatctgcacc cactgggant 250
 tntataggaa caatcatggc atatgataat gacataggag agaatgcaga 300
 aatggattac agcattgaag aggatgattc gcaaacattt gacattatt 349

<210> 266
 <211> 25
 <212> DNA
 <213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 266

cttgactgtc tctgaatctg caccc 25

<210> 267

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 267

aagtgggtgga agcctccagt gtgg 24

<210> 268

<211> 52

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 268

ccactacggt attagagcaa aagttaaaaa ccatcatggt tcctggagca 50

gc 52

<210> 269

<211> 2747

<212> DNA

<213> Homo sapiens

<400> 269

gcaacctcag cttctagtat ccagactcca gcgccgcccc gggcgcgga 50

cccaaccccc acccagagct tctccagcgg cgccgcagcg agcagggctc 100

cccgccctaa cttcctccgc ggggccagc caccttcggg agtccgggtt 150

gccacctgc aaactctccg ctttctgcac ctgccacccc tgagccagcg 200

cgggcccccg agcgagtcac ggccaacgcg gggctgcagc tgttgggctt 250

cattctcgcc ttcctgggat ggatcggcgc catcgtcagc actgccctgc 300

cccagtggag gatttactcc tatgccggcg acaacatcgt gaccgcccag 350

gccatgtacg aggggctgtg gatgtcctgc gtgtcgcaga gcaccgggca 400

gatccagtgc aaagtctttg actccttgct gaatctgagc agcacattgc 450

aagcaacccg tgccttgatg gtgggttgga tcctcctggg agtgatagca 500

atctttgtgg ccaccgttgg catgaagtgt atgaagtgc tgggaagacga 550

tgaggtgcag aagatgagga tggctgtcat tgggggtgcg atatttcttc 600

ttgcaggctct ggctattttta gttgccacag catggtatgg caatagaatc 650
 gttcaagaat tctatgaccc tatgacccca gtcaatgccca ggtacgaatt 700
 tggtcaggct ctcttcaactg gctgggctgc tgcttctctc tgccttctgg 750
 gaggtgccct actttgctgt tctgtcccc gaaaaacaac ctcttaccga 800
 acaccaaggc cctatccaaa acctgcacct tccagcggga aagactacgt 850
 gtgacacaga ggcaaaagga gaaaatcatg ttgaaacaaa ccgaaaatgg 900
 acattgagat actatcatta acattaggac cttagaattt tgggtattgt 950
 aatctgaagt atggtattac aaaacaaaca aacaaacaaa aaacccatgt 1000
 gttaaaatac tcagtgctaa acatggctta atcttatttt atcttctttc 1050
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 gtaatcatac tcaaattgggg gaaggggtgc tccttaaata tatatagata 1150
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 cattatgttg atactagcat acttaaaata tctctaaaat aggtaaatgt 1250
 atttaattcc atattgatga agatgtttat tgggtatatt tctttttcgt 1300
 ccttatatac atatgtaaca gtcaaatac atttactctt cttcattagc 1350
 tttgggtgcc tttgccacaa gacctagcct aatttaccaa ggatgaattc 1400
 tttcaattct tcatgctgc ctttttcata tacttatttt attttttacc 1450
 ataatcttat agcacttgca tcgttattaa gcccttattt gttttgtggt 1500
 tcattggtct ctatctcctg aatctaacac atttcatagc ctacatttta 1550
 gtttctaaag ccaagaagaa tttattacaa atcagaactt tggaggcaaa 1600
 tctttctgca tgaccaaagt gataaattcc tgttgacctt cccacacaat 1650
 ccctgtactc tgacccatag cactcttggt tgccttgaaa atatttgtcc 1700
 aattgagtag ctgcatgctg ttccccagg tgttgtaaca caactttatt 1750
 gattgaattt ttaagctact tattcatagt tttatatccc cctaaactac 1800
 ctttttggtc cccattcctt aattgtattg ttttcccaag tgtaattatc 1850
 atgcgtttta tatcttcta ataaggtgtg gtctgtttgt ctgaacaaag 1900
 tgctagactt tctggagtga taatctggtg acaaattatc tctctgtagc 1950
 tgtaagcaag tcacttaatc tttctacctc ttttttctat ctgccaaatt 2000
 gagataatga tacttaacca gttagaagag gtagtgtgaa tattaattag 2050

tttatattac tcttattctt tgaacatgaa ctatgcctat gtagtgtctt 2100
tatttgctca gctggctgag aactgaaga agtcactgaa caaacctac 2150
acacgtacct tcatgtgatt cactgccttc ctctctctac cagtctatctt 2200
ccactgaaca aaacctacac acataccttc atgtggttca gtgccttctt 2250
ctctctacca gtctatttcc actgaacaaa acctacgcac ataccttcat 2300
gtggctcagt gccttctctt ctctaccagt ctatttccat tctttcagct 2350
gtgtctgaca tgtttgtgct ctgttccatt ttaacaactg ctcttacttt 2400
tccagtctgt acagaatgct atttcacttg agcaagatga tgtaatggaa 2450
agggtgttgg cactggtgtc tggagacctg gatttgagtc ttggtgctat 2500
caatcacctg ctgtgtttga gcaaggcatt tggctgctgt aagcttattg 2550
cttcatctgt aagcgggtgg ttgtaattcc tgatcttccc acctcacagt 2600
gatgttgtgg ggatccagtg agatagaata catgtaagtg tggttttgta 2650
atttaaaaag tgctatacta agggaaagaa ttgaggaatt aactgcatac 2700
gttttggtgt tgcttttcaa atgtttgaaa ataaaaaaaaa tgttaag 2747

<210> 270
<211> 211
<212> PRT
<213> Homo sapiens

<400> 270
Met Ala Asn Ala Gly Leu Gln Leu Leu Gly Phe Ile Leu Ala Phe
1 5 10 15
Leu Gly Trp Ile Gly Ala Ile Val Ser Thr Ala Leu Pro Gln Trp
20 25 30
Arg Ile Tyr Ser Tyr Ala Gly Asp Asn Ile Val Thr Ala Gln Ala
35 40 45
Met Tyr Glu Gly Leu Trp Met Ser Cys Val Ser Gln Ser Thr Gly
50 55 60
Gln Ile Gln Cys Lys Val Phe Asp Ser Leu Leu Asn Leu Ser Ser
65 70 75
Thr Leu Gln Ala Thr Arg Ala Leu Met Val Val Gly Ile Leu Leu
80 85 90
Gly Val Ile Ala Ile Phe Val Ala Thr Val Gly Met Lys Cys Met
95 100 105
Lys Cys Leu Glu Asp Asp Glu Val Gln Lys Met Arg Met Ala Val
110 115 120

Ile Gly Gly Ala	Ile Phe Leu Leu Ala	Gly Leu Ala	Ile Leu Val
125		130	135
Ala Thr Ala Trp	Tyr Gly Asn Arg Ile	Val Gln Glu Phe Tyr Asp	
140		145	150
Pro Met Thr Pro	Val Asn Ala Arg Tyr	Glu Phe Gly Gln Ala Leu	
155		160	165
Phe Thr Gly Trp	Ala Ala Ala Ser Leu	Cys Leu Leu Gly Gly Ala	
170		175	180
Leu Leu Cys Cys	Ser Cys Pro Arg Lys	Thr Thr Ser Tyr Pro Thr	
185		190	195
Pro Arg Pro Tyr	Pro Lys Pro Ala Pro	Ser Ser Gly Lys Asp Tyr	
200		205	210

Val

<210> 271
 <211> 564
 <212> DNA
 <213> Homo sapiens

<220>
 <221> unsure
 <222> 21, 69, 163, 434, 436, 444
 <223> unknown base

<400> 271
 ttctggccaa acccggggct ncagctgttg ggcttcatct cgccttcctg 50
 ggatggatcg gcgccatcnt cacactgccc ttccccagtg gaggatttta 100
 ctccctatgc tggcgacaac atcgtgaccg cccagcccat gtacgagggg 150
 ctgtggatgt ccngcgtgtc gcagagcacc gggcagatcc agtgcaaagt 200
 ctttgactcc ttgctgaatc tgagcagcac attgcaagca acccgtgcct 250
 tgatggtggt tggcatcctc ctgggagtga tagcaatctt tgtggccacc 300
 gttggcatga agtgtatgaa gtgcttgga gacgatgagg tgcagaagat 350
 gaggatggct gtcattgggg gcgcgatatt tcttcttgca ggtctggcta 400
 ttttagttgc cacagcatgg tatggcaata gaancnttca acanttttat 450
 gaccctatga cccagtc aa tgccaggtac gaatttggtc aggcctctctt 500
 cactggctgg gctgctgctt ctctctgcct tctgggaggt gccctacttt 550
 gctgttcctg tccc 564

<210> 272
 <211> 498

<212> DNA
<213> Homo sapiens

<220>
<221> unsure
<222> 30, 49, 102, 141, 147, 171, 324-325, 339-341
<223> unknown base

<400> 272
acccttgacc caacgcggcc ccccgaccgn ttcattggcca aacgcgggnc 50
tccagctggtt gggcttcatt ctccccctcc tgggatggac cggcgcccat 100
cntcagcact gccctgcccc agtggaggat ttactcctat nccggcnaca 150
acatcgtgac cgcccaggcc ntgtacgagg ggctgtggat gtccctgcgtg 200
tcgcagagca ccgggcagat ccagtgcata gtctttgact cctttgctga 250
atctgagcag cacattgcaa gcaaccctgt ccttgatggt gggttggcatc 300
ctcctgggag tgatagcaat cttnttggcc accgttgtnn ntgaagtga 350
tgaagtgctt ggaagacgat gaggtgcaga agatgaggat ggctgtcatt 400
gggggcgaga tttttcttct tgcaggtctg gctatttttag ttgccacagc 450
atggtatggc aatagaatcg ttcaagaatt ctatgaccct atgaccga 498

<210> 273
<211> 552
<212> DNA
<213> Homo sapiens

<220>
<221> unsure
<222> 25, 57, 67, 94-95, 116, 152, 165, 212, 233, 392-394
<223> unknown base

<400> 273
gggcccgaacc attatccaac cgggntcact gttggctcat ctccctcctg 50
gatgaancgc gccatcntca gactccctgc cccatggaga tttnnccat 100
gctggcgaca acatcntgac cccagccat gtacgagggg ctttgaacgt 150
cngcgtgtcg cagancaccg ggcagatcca gtgcaaagtc tttgactcct 200
tgctgaatct gngcagcaca ttgcagcaac cnttgccctg atggtgggtg 250
gcatcctcct gggagtgaata gcaatctttg tggccaccgt tggcatgaag 300
tgtatgaagt gcttgaaga cgatgaggtg cagaagatga ggatggctgt 350
cattgggggc gcgatatttc ttcttgacag tctggctatt tnnngttgcc 400
acagcatggt atggcaatag aatcgttcaa gaattctatg accctatgac 450

cccagtcagt gccaggtacg aatttgggtca ggctctcttc actgggtggg 500
 ctgctgcttc tctctgcctt ctgggaggtg ccctactttg ctgttcctgc 550
 ga 552

<210> 274
 <211> 526
 <212> DNA
 <213> Homo sapiens
 <220>
 <221> unsure
 <222> 25, 50, 60, 123, 127, 370, 395, 397-398, 402-403, 405-407
 <223> unknown base

<400> 274
 attctcccct cctggatgga tgcgccacc gtcacattgc cttccccan 50
 tggaggattn actcctatgc tggcgacaac atcgtgacct cccaggccat 100
 ttaccgaggg gctttggatg tcttgctgtg cgcagagcac cgggcagatc 150
 ccagtgcata gtctttgact ccttgctgaa tctgagcagc acattgcaag 200
 caaccctgct cttgatgggg ttggcatcct cctgggagtg atagcaacct 250
 ttgtggccac cgttggcatg aagtgtatga agtgcttggg agacgatgag 300
 gtgccagaag atgaggatgg ctgtcattgg gggcgcgata tttcttggtg 350
 caggtctggc tatttttagtn gccacagcat ggtatggcaa tagantnntt 400
 cnnngnnntct atgacctat gaccocagtc aatgccaggt acgaatttgg 450
 tcaggctctc ttactgggtt gggctgctgc ttctctctgc cttctgggag 500
 gtgccctact ttgctgttcc tgtccc 526

<210> 275
 <211> 398
 <212> DNA
 <213> Homo sapiens
 <220>
 <221> unsure
 <222> 22, 61, 91, 144, 238-239, 262, 265-266, 271, 274
 <223> unknown base

<400> 275
 agagcaccgg cagatcccag tncaaagtct ttgaccttg ctgaatctga 50
 gcagcacatt ncaagcaacc ccttgccctg aagggtggtg ncatcccccc 100
 tgggagtgaa tagcaatctt tgtggccacc gttggcatga agtntatgaa 150
 gtgcttggaa gacgatgagg tgcagaagat gaggatggct gtcattgggg 200

gcgcgatatt tcttcttgca ggtctggcta ttttagtnnc cacagcatgg 250
 tatggcaata gnatnnttcg nggnttctat gaccctatga cccagtcaa 300
 tgccaggtag gaatttggtc aggctctctt cactggctgg gctgctgctt 350
 ctctctgcct tctgggaggt gccctacttt gctgttctg tccccgaa 398

<210> 276
 <211> 495
 <212> DNA
 <213> Homo sapiens

<220>
 <221> unsure
 <222> 39, 58, 130, 234, 314, 364, 427, 450, 461, 476
 <223> unknown base

<400> 276
 agcaatgccc tgccccaggt ggaggattaa ttcctatgnt ggggacaaca 50
 ttgtgacngc ccaggccatg tacggggggc tgtggatgtc ctgcgtgtcg 100
 cagagcaccg ggcagatcca gtgcaaagtn tttgactcct tgctgaattt 150
 gagcagcaca ttgcaagcaa cccgtgcctt gatggtgggt ggcatcttcc 200
 tgggagtgat agcaatcttt gtggccaccg tggnaatgaa gtgtatgaag 250
 tgcttggaag acgatgaggt gcagaagatg aggatggctg tcattggggg 300
 gcgcgatattt cttnttgacg gtctggctat tttagttgcc acagcatggt 350
 atggcaatag aatngttcaa gaattttatg accctatgac cccagtcaat 400
 gccaggtagc aatttggtca ggctttnttc actggctggg ctgctgcttn 450
 tttctgcctt ntgggaggtg ccctantttg ctgttctctg gaacc 495

<210> 277
 <211> 200
 <212> DNA
 <213> Homo sapiens

<220>
 <221> unsure
 <222> 34, 87, 138, 147, 163, 165-166, 172
 <223> unknown base

<400> 277
 tcataggggg gcgcgatatt ttttcttgca ggtntgggta ttttagttgc 50
 cacagcatgg tatggcaata gaatcggtca agaattntat gaccctatga 100
 cccagtcaa tgccaggtag gaatttggtc aggctctntt cactggntgg 150
 gctgctgctt ctntnngcct tntgggaggt gccctacttt gctgttctg 200

<210> 278
<211> 542
<212> DNA
<213> Homo sapiens

<220>
<221> unsure
<222> 26, 43, 55, 77, 198, 361-362, 391-392, 396
<223> unknown base

<400> 278
ttcctgggat ggatccgccc ccatcntcac atgccctgcc cnttggagat 50
ttacncctat gctggcgaac aacatcntga ccgcccaggc catgtacgag 100
gggctgtgga atgtcctgcg tgtcccagag caccgggcag atccagtgc 150
aagtctttga ctcccttgctg aatctgagca gcacattgca agcaaccntg 200
ccttgatggg ggttggcatc ctccctgggag tgatagcaat ctttgtggcc 250
accgttggca tgaaagtgtg tgaagtgtt ggaagacgat gaggtgcaga 300
agatgaggat ggctgtcatt gggggcgcgga tatttcttct tgcaggtctg 350
gctatttttag nngccacagc atgggtatggc aatcagaccc nntcanaaac 400
tctatgaccc tatgacccca gtcaatgccg ggtacgaatt tggtcaggct 450
ctcttcactg gctgggctgc tgcttctctc tgccttcttg gaggtgccct 500
actttgtgtg tctgtcccc gaaaaacaac ctcttaccga cg 542

<210> 279
<211> 548
<212> DNA
<213> Homo sapiens

<220>
<221> unsure
<222> 90, 115, 147, 228, 387
<223> unknown base

<400> 279
cggggctgca gctgttgggc ttcactctgc ttccctgggat ggaatcggcg 50
ccatcgtcag cactgccctg ccccatggag gatttactcn tatgctggcg 100
acaacatcgt gaccncccag gccatgtacg aggggctgtg gatgtcngcg 150
tgtcgagag caccgggcag atccagtgc aagtctttga ctcccttgctg 200
aatctgagca gcacattgca agcaaccntg ccttgatggg ggttggcatc 250
ctccctgggag tgatagcaat ctttgtggcc accgttggca tgaagtgtat 300
gaagtgttg gaagacgatg aggtgcagaa gatgaggatg gctgtcattg 350

ggggcgcgat atttcttctt gcaggtctgg ctatttntag ttgccacagc 400
atgggtatggc aatagaatcg ttcaagaatt ctatgaccct atgaccccag 450
tcaatgccag gtacgaattt ggtcaggctc tcttcactgg ctgggctgct 500
gcttctctct gccttctggg aggtgcccta ctttctgtt cctgcgaa 548

<210> 280

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 280

cgagcgagtc atggccaacg c 21

<210> 281

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 281

gtgtcacacg tagtctttcc cgctgg 26

<210> 282

<211> 43

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 282

ctgcagctgt tgggcttcat tctgccttc ctgggatgga tcg 43

<210> 283

<211> 2285

<212> DNA

<213> Homo sapiens

<400> 283

gcgtgccgtc agctcgccgg gcaccgaggc ctgcacctcg cctccggccc 50

ctgcgcctgc accgcgtaga ccgaccccc cctccagcgc gcccacccgg 100

tagaggaccc ccgcccgtgc cccgaccggt ccccgccctt ttgtaaaact 150

taaagcgggc gcagcattaa cgcttccgc cccggtgacc tctcaggggt 200

ctccccgcca aagggtgctcc gccgctaagg aacatggcga aggtggagca 250

ggtcctgagc ctcgagccgc agcacgagct caaattccga ggtcccttca 300

ctctgttggg tgaactggta ttgctgctgg agggctgtgg gctcctctgt 1800
ctctggagag tctggatcatg tggaggtggg gtttattggg atgctggaga 1850
agagctgccca ggaagtgttt tttctgggtc agtaaataac aactgtcata 1900
gggagggaaa ttctcagtag tgacagtcaa ctctaggtta ccttttttaa 1950
tgaagagtag tcagtcttct agattgttct tataccacct ctcaaccatt 2000
actcacactt ccagcgccca ggtccaagtc tgagcctgac ctccccttgg 2050
ggacctagcc tggagtcagg acaaatggat cgggctgcag agggttagaa 2100
gcgagggcac cagcagttgt ggggtggggag caaggggaaga gagaaactct 2150
tcagcgaatc cttctagtag tagttgagag tttgactgtg aattaatttt 2200
atgccataaa agaccaaccc agttctgttt gactatgtag catcttgaaa 2250
agaaaaatta taataagcc ccaaaattaa gaaaa 2285

<210> 284
<211> 243
<212> PRT
<213> Homo sapiens

<400> 284
Met Ala Lys Val Glu Gln Val Leu Ser Leu Glu Pro Gln His Glu
1 5 10 15
Leu Lys Phe Arg Gly Pro Phe Thr Asp Val Val Thr Thr Asn Leu
20 25 30
Lys Leu Gly Asn Pro Thr Asp Arg Asn Val Cys Phe Lys Val Lys
35 40 45
Thr Thr Ala Pro Arg Arg Tyr Cys Val Arg Pro Asn Ser Gly Ile
50 55 60
Ile Asp Ala Gly Ala Ser Ile Asn Val Ser Val Met Leu Gln Pro
65 70 75
Phe Asp Tyr Asp Pro Asn Glu Lys Ser Lys His Lys Phe Met Val
80 85 90
Gln Ser Met Phe Ala Pro Thr Asp Thr Ser Asp Met Glu Ala Val
95 100 105
Trp Lys Glu Ala Lys Pro Glu Asp Leu Met Asp Ser Lys Leu Arg
110 115 120
Cys Val Phe Glu Leu Pro Ala Glu Asn Asp Lys Pro His Asp Val
125 130 135
Glu Ile Asn Lys Ile Ile Ser Thr Thr Ala Ser Lys Thr Glu Thr
140 145 150

Pro Ile Val Ser Lys Ser Leu Ser Ser Ser Leu Asp Asp Thr Glu
155 160 165

Val Lys Lys Val Met Glu Glu Cys Lys Arg Leu Gln Gly Glu Val
170 175 180

Gln Arg Leu Arg Glu Glu Asn Lys Gln Phe Lys Glu Glu Asp Gly
185 190 195

Leu Arg Met Arg Lys Thr Val Gln Ser Asn Ser Pro Ile Ser Ala
200 205 210

Leu Ala Pro Thr Gly Lys Glu Glu Gly Leu Ser Thr Arg Leu Leu
215 220 225

Ala Leu Val Val Leu Phe Phe Ile Val Gly Val Ile Ile Gly Lys
230 235 240

Ile Ala Leu

<210> 285
<211> 418
<212> DNA
<213> Homo sapiens

<220>
<221> unsure
<222> 40, 53, 68, 119, 134, 177-178, 255
<223> unknown base

<400> 285
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tcnagcgcgcc aggtccangt ctgagcctga cttccccttg gggacctagc 100
ctggagtcag gacaatggnt cgggctgcag aggnntagaa gcgagggcac 150
cagcagtttt ggggtggggag caagggngga gagaaactct tcagcgaatc 200
cttctagtag tagttgagag tttgactgtg aattaatttt atgccataaa 250
agacnaaccc agttctgttt gactatgtag catcttgaaa agaaaaatta 300
taataaagcc ccaaaattaa gaattctttt gtcattttgt cacatttgct 350
ctatgggggg aattattatt ttatcatttt tattattttg ccattggaag 400
gttaacttta aaatgagc 418

<210> 286
<211> 543
<212> DNA
<213> Homo sapiens

<220>
<221> unsure
<222> 73, 97

<223> unknown base

<400> 286

tattgtaaaag gccatttttaa accatttgga ggccttgga catgatgctg 50
gattacctcc ttaaattgaca ccttcctcg cctgttggtg ctggccttg 100
gggagctgga gccccagcat gctggggagt gcggtcagct ccacacagta 150
gtccccacgt ggcccaactcc cggcccaggc tgctttccgt gtcttcagtt 200
ctgtccaagc catcagctcc ttgggactga tgaacagagt cagaagccca 250
aaggaattgc cactgtggca gcatcagacg tactcgtcat aagtgagagg 300
cgtgtgttga ctgattgacc cagcgctttg gaaataaatg gcagtgtttt 350
gttcacttaa agggaccaag ctaaattgta ttggttcag tagtgaagtc 400
aaactgttat tcagagatgt ttaatgcata ttaacttat ttaatgtatt 450
tcattctatg ttttcttatt gtcacaagag tacagttaat gctgcgtgct 500
gctgaactct gttgggtgaa ctggtattgc tgctggaggg ctg 543

<210> 287

<211> 270

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> 38, 64, 72, 164, 198, 200, 220, 222, 229, 242

<223> unknown base

<400> 287

ccctgggtggt tttgttcttt aattcgttg tgtaattntt gggaagattg 50
cttgtagagg tagnatgcac cnggctgga aattggattg gtggatccac 100
catatccatg ggattttaaat ttatcataac catgtgtaaa aagaaattaa 150
tgtatgatga catntcacag gtattgcctt taaattaccc atccctgnan 200
acacatacac agatacacan anacaaatnt aatgtaacga tnttttagaa 250
agttaaaaat gtatagtaac 270

<210> 288

<211> 428

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> 35, 116, 129, 197, 278, 294, 297, 349, 351

<223> unknown base

<400> 288
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 gccatcagct ccttgggact gatgaacaga gtcagaagcc caaaggaatt 100
 gcaactgtggc agcatnagac gtacttgtna taagtgagag gcgtgtgttg 150
 actgattgac ccagcgcttt ggaaataaat ggcagtgtt tgttcantta 200
 aagggaacaa gctaaatttg tattggttca ttagtggaag tcaaactgtt 250
 attcagagat gtttaattgca tatttaantt atttaattga tttnatntca 300
 tgttttctta ttgtcacaag agtacagtta atgctgcgtg ctgctgaant 350
 ntgttgggtg aactggtatt gctgctggag ggctgtgggc tcctctgtct 400
 ttggagagtc tggatcatgtg gaggtggg 428

<210> 289
 <211> 320
 <212> DNA
 <213> Homo sapiens

<400> 289
 tgctttccgt gtcttcagtt ctgtccaagc catcagctcc ttgggacttg 50
 atgaacagag tcagaagccc aaaggaattg cactgtggca gcatcagacg 100
 tactogtcat aagtgaagag cgtgtgttga ctgattgacc cagcgctttg 150
 gaaataaatg gcagtgtttt gttcacttaa agggaccaag cttaaatttg 200
 attggttcat gtagtgaagt caaactgtta ttcagagatg ttttaattgat 250
 atttaactta ttttaattgat ttcattctcat gttttcttat tgtcacaaga 300
 gtacagttaa tgctgcgtgc 320

<210> 290
 <211> 609
 <212> DNA
 <213> Homo sapiens

<220>
 <221> unsure
 <222> 57, 60, 186, 235, 244, 304, 339, 355, 359, 361, 387, 432, 441,
 447, 481, 513, 532, 584, 598
 <223> unknown base

<400> 290
 aaacctttta aagttgagg gaaaagaatg atcctttatt aatgacaagg 50
 gaaacnctgn gtaatgccac aatggcatat tgtaaattgc attttaaaca 100
 ttggtaggcc ttggtacatg atgctggatt acctctotta aaatgacacc 150
 cttctctgcc tgttgggtgc ggcccttggg gagctngagc ccagcatgct 200

ggggagtgcg gttctgtcca cacagtagtc cccangtggc ccantcccgg 250
 cccaggctgc tttccgtgtc ttcagttctg tccaagccat cagctccttg 300
 ggantgatga acagagtcag aagcccaaag gaattgcant gtggcagcat 350
 cagangtant ngtcataagt gagaggcgtg tgttgantga ttgaccagc 400
 gctttggaaa taaatggcag tgctttgttc anttaaaggg nccaagntaa 450
 atttgtattg gttcatgtag tgaagtcaaa ntgttattca gagatgttta 500
 atgcatattt aanttattta atgtatttca tntcatgttt tottattgtc 550
 acaagggtac agttaatgct gcgtgctgct gaantctgtt gggatgaantg 600
 gtattgctg 609

<210> 291
 <211> 493
 <212> DNA
 <213> Homo sapiens

<400> 291
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 cacagtagtc cccacgtggc ccactcccgg cccaggctgc tttccgtgtc 100
 ttcagttctg tccaagccat cagctccttg ggactgatga acagagtcag 150
 aagcccaaag gaattgcact gtggcagcat cagacgtact cgtcataagt 200
 gagaggcgtg tgttgactga ttgaccagc gctttggaaa taaatggcag 250
 tgctttgttc acttaaaggg accaagctaa atttgtattg gttcatgtag 300
 tgaagtcaaa ctgttattca gagatgttta atgcatattt aacttattta 350
 atgtatttca tctcatgttt tottattgtc acaagagtac agttaatgct 400
 gcgtgctgct gaactctgtt gggatgaactg gtattgctgc tggagggtg 450
 tgggctcctc tgtctctgga gactctggc atgtggaggt ggg 493

<210> 292
 <211> 27
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 292
 gcaccaccgt aggtacttgt gtgaggc 27

<210> 293
 <211> 23
 <212> DNA

[illegible]

<223> Synthetic oligonucleotide probe

aaccaccaga gccaaagagcc ggg 23

<211> 50

<213> Artificial Sequence

<223> Synthetic oligonucleotide probe

cagcggaaatc atcgatgcag gggcctcaat taatgtatct gtgatgttac 50

<211> 2530

<213> Homo sapiens

gcgagctccg ggtgctgtgg cccggccttg gcggggcggc ctccgactca 50

ggctggctga gaggtccca gctgcagcgt cccgcccgc ctctcagga 100

gctctgatct cagctgacag tgccctcggg gaccaaaca gacctggcagg 150

gtctcacttt gttgccagc ctggaattca gtgcatgat catgatttac 200

tgcagccttg acctcctggg ttcaagcgat cctgctgagt agctgggact 250

acaggacaaa attagaagat caaaatqgaa aatatgctgc tttgattgat 300

atttttcacc cctgggtgga ccctcattga tggatctgaa atggaatggg 350

at tt t t a t g t g g c a c t t g a g a a a g g t a c c c c g g a t t g t c a g t g a a a g g a c t 400

ttccatctca ccagcccccgc atttgaggca gatgctaaga tgatggtaaa 450

tacagtgtgt ggcacgaat gccagaaaga actcccaact cccagccttt 500

ctgaattgga ggattatctt tcctatgaga ctgtctttga gaatggcacc 550

cgaaccttaa ccagggtgaa agttcaagat ttgattcttg agccgactca 600

aaatatcacc acaaagggag tatctgttag gagaaagaga caggtgtatg 650

gcaccgacag caggttcagc atcttggaca aaaggttctt aaccaatttc 700

cctttcagca cagctgtgaa gctttccacg ggctgtagtg gcatttctcat 750

ttccctcag catgttctaa ctgctgccca ctgtgttcat gatggaaaag 800

actatgtcaa agggagtaaa aagctaaggg tagggttqtt gaagatgagg 850

aataaaagtg gaggcaagaa acgtcgaggt tctaagagga gcaggagaga 900
agctagtggg ggtgaccaaa gagaggggtac cagagagcat ctgcaggaga 950
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tccgaagggc tgggcacgag gaggcattggg ggacgctacc ttggactatg 1100
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gtgggcactt caatgccaaag tatatactct tctttacatg gtgatgagtt 1750
tcattttagt aaaaattttg ttgccttctt aaaaattaga cacactttaa 1800
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ctcagggtcc tactctaaga agaatactaat aggatgctgg ttgtgtatta 1900
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atagagacag aaagttacaa cacagtttgt actactctga gatggatcca 2000
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catttagttt agtttttttg aagaattaca aatcagaaga aaaagcaagc 2100
attataaaca aaactaataa ctgttttact gctttaagaa ataacaatta 2150
caatgtgtat tatttaaaaa tgggagaaat agtttgttct atgaaataaa 2200
cctagtttag aaatagggaa gctgagacat tttaagatct caagttttta 2250
tttaactaat actcaaaata tggacttttc atgtatgcat agggaagaca 2300

cttcacaaat tatgaatgat catgtgttga aagccacatt attttatgct 2350
 atacattcta tgtatgaggt gctacatttt taggacaaag aattctgtaa 2400
 tctttttcaa gaaagagtct ttttctcctt gacaaaatcc agcttttgta 2450
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 cctaaaaatg aataaaattt atgaatatga 2530

<210> 296
 <211> 413
 <212> PRT
 <213> Homo sapiens

<400> 296

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Thr	Leu	Ile	Asp	Gly	Ser	Glu	Met	Glu	Trp	Asp	Phe	Met	Trp	His	
				20					25					30	
Leu	Arg	Lys	Val	Pro	Arg	Ile	Val	Ser	Glu	Arg	Thr	Phe	His	Leu	
				35					40					45	
Thr	Ser	Pro	Ala	Phe	Glu	Ala	Asp	Ala	Lys	Met	Met	Val	Asn	Thr	
				50					55					60	
Val	Cys	Gly	Ile	Glu	Cys	Gln	Lys	Glu	Leu	Pro	Thr	Pro	Ser	Leu	
				65					70					75	
Ser	Glu	Leu	Glu	Asp	Tyr	Leu	Ser	Tyr	Glu	Thr	Val	Phe	Glu	Asn	
				80					85					90	
Gly	Thr	Arg	Thr	Leu	Thr	Arg	Val	Lys	Val	Gln	Asp	Leu	Val	Leu	
				95					100					105	
Glu	Pro	Thr	Gln	Asn	Ile	Thr	Thr	Lys	Gly	Val	Ser	Val	Arg	Arg	
				110					115					120	
Lys	Arg	Gln	Val	Tyr	Gly	Thr	Asp	Ser	Arg	Phe	Ser	Ile	Leu	Asp	
				125					130					135	
Lys	Arg	Phe	Leu	Thr	Asn	Phe	Pro	Phe	Ser	Thr	Ala	Val	Lys	Leu	
				140					145					150	
Ser	Thr	Gly	Cys	Ser	Gly	Ile	Leu	Ile	Ser	Pro	Gln	His	Val	Leu	
				155					160					165	
Thr	Ala	Ala	His	Cys	Val	His	Asp	Gly	Lys	Asp	Tyr	Val	Lys	Gly	
				170					175					180	
Ser	Lys	Lys	Leu	Arg	Val	Gly	Leu	Leu	Lys	Met	Arg	Asn	Lys	Ser	
				185					190					195	
Gly	Gly	Lys	Lys	Arg	Arg	Gly	Ser	Lys	Arg	Ser	Arg	Arg	Glu	Ala	
				200					205					210	

Ser	Gly	Gly	Asp	Gln 215	Arg	Glu	Gly	Thr	Arg 220	Glu	His	Leu	Gln	Glu 225
Arg	Ala	Lys	Gly	Gly 230	Arg	Arg	Arg	Lys	Lys 235	Ser	Gly	Arg	Gly	Gln 240
Arg	Ile	Ala	Glu	Gly 245	Arg	Pro	Ser	Phe	Gln 250	Trp	Thr	Arg	Val	Lys 255
Asn	Thr	His	Ile	Pro 260	Lys	Gly	Trp	Ala	Arg 265	Gly	Gly	Met	Gly	Asp 270
Ala	Thr	Leu	Asp	Tyr 275	Asp	Tyr	Ala	Leu	Leu 280	Glu	Leu	Lys	Arg	Ala 285
His	Lys	Lys	Lys	Tyr 290	Met	Glu	Leu	Gly	Ile 295	Ser	Pro	Thr	Ile	Lys 300
Lys	Met	Pro	Gly	Gly 305	Met	Ile	His	Phe	Ser 310	Gly	Phe	Asp	Asn	Asp 315
Arg	Ala	Asp	Gln	Leu 320	Val	Tyr	Arg	Phe	Cys 325	Ser	Val	Ser	Asp	Glu 330
Ser	Asn	Asp	Leu	Leu 335	Tyr	Gln	Tyr	Cys	Asp 340	Ala	Glu	Ser	Gly	Ser 345
Thr	Gly	Ser	Gly	Val 350	Tyr	Leu	Arg	Leu	Lys 355	Asp	Pro	Asp	Lys	Lys 360
Asn	Trp	Lys	Arg	Lys 365	Ile	Ile	Ala	Val	Tyr 370	Ser	Gly	His	Gln	Trp 375
Val	Asp	Val	His	Gly 380	Val	Gln	Lys	Asp	Tyr 385	Asn	Val	Ala	Val	Arg 390
Ile	Thr	Pro	Leu	Lys 395	Tyr	Ala	Gln	Ile	Cys 400	Leu	Trp	Ile	His	Gly 405
Asn	Asp	Ala	Asn	Cys 410	Ala	Tyr	Gly							

<210> 297

<211> 24

<212> DNA

<213> Artificial Sequence

$\langle 220 \rangle$

<223> Synthetic oligonucleotide probe

<400> 297

gcatctgcag gagagagcga aggg 24

<210> 298

<211> 24

<212> DNA

<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 298
catcggtccc gtgaatccag aggc 24

<210> 299
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 299
gaaggaggc cttcctttca gtggaccccg gtcaagaata ccac 45

<210> 300
<211> 1869
<212> DNA
<213> Homo sapiens

<400> 300
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ccagtactgg atgtgacagc aggcagagga gcacttagca gcttattcag 100
tgtccgattc tgattccggc aaggatccaa gcatggaatg ctgccgtcgg 150
gcaactcctg gcacactgct cctctttctg gctttcctgc tctgagttc 200
caggaccgca cgctccgagg aggaccggga cggcctatgg gatgcctggg 250
gcccatggag tgaatgctca cgcacctgag ggggaggggc ctctactct 300
ctgaggcgct gcctgagcag caagagctgt gaaggaagaa atatccgata 350
cagaacatgc agtaatgtgg actgccacc agaagcagggt gatttccgag 400
ctcagcaatg ctcagctcat aatgatgtca agcaccatgg ccagttttat 450
gaatggcttc ctgtgtctaa tgaccctgac aacctatgtt cactcaagtg 500
ccaagccaaa ggaacaaccc tgggtgttga actagcacct aaggctcttag 550
atggtaacgg ttgctataca gaatctttgg atatgtgcat cagtggttta 600
tgccaaattg ttggctgcga tcaccagctg ggaagcaccg tcaaggaaga 650
taactgtggg gtctgcaacg gagatgggtc cacctgccgg ctgggccgag 700
ggcagtataa atcccagctc tccgcaacca aatcgatga tactgtggtt 750
gcacttccct atggaagtag acatattcgc cttgtcttaa aaggctcctga 800
tcacttatat ctggaacca aaaccctcca ggggactaaa ggtgaaaaca 850
gtctcagctc cacaggaact ttccttgggg acaattctag tgtggacttc 900

350	355	360
Ala Ser Asp Gly Tyr Lys Gln Ile Met	Pro Tyr Asp Leu Tyr His	
365	370	375
Pro Leu Pro Arg Trp Glu Ala Thr Pro	Trp Thr Ala Cys Ser Ser	
380	385	390
Ser Cys Gly Gly Gly Ile Gln Ser Arg	Ala Val Ser Cys Val Glu	
395	400	405
Glu Asp Ile Gln Gly His Val Thr Ser	Val Glu Glu Trp Lys Cys	
410	415	420
Met Tyr Thr Pro Lys Met Pro Ile Ala	Gln Pro Cys Asn Ile Phe	
425	430	435
Asp Cys Pro Lys Trp Leu Ala Gln Glu	Trp Ser Pro Cys Thr Val	
440	445	450
Thr Cys Gly Gln Gly Leu Arg Tyr Arg	Val Val Leu Cys Ile Asp	
455	460	465
His Arg Gly Met His Thr Gly Gly Cys	Ser Pro Lys Thr Lys Pro	
470	475	480
His Ile Lys Glu Glu Cys Ile Val Pro	Thr Pro Cys Tyr Lys Pro	
485	490	495
Lys Glu Lys Leu Pro Val Glu Ala Lys	Leu Pro Trp Phe Lys Gln	
500	505	510
Ala Gln Glu Leu Glu Glu Gly Ala Ala	Val Ser Glu Glu Pro Ser	
515	520	525

<210> 302
 <211> 1533
 <212> DNA
 <213> Homo sapiens

<400> 302
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 ctcgggcctg acagatggca gtggccactg cggcggcagt actggccgct 100
 ctgggcgggg cgctgtggct ggcggcccg cggttcgtgg ggcccagggt 150
 ccagcggctg cgcagaggcg gggaccccg cctcatgcac gggaagactg 200
 tgctgatcac cggggcgaac agcggcctgg gccgcgccac ggccgccgag 250
 ctactgcgcc tgggagcgcg ggtgatcatg ggctgccggg accgcgcgcg 300
 cgccgaggag ggcgggggtc agctccgccg cgagctccgc caggccgcgg 350
 agtgcgggcc agagcctggc gtcagcgggg tgggcgagct catagtccgg 400
 gagctggacc tcgcctcgct gcgctcgggt cgcgccttct gccaggaaat 450

gctccaggaa gagcctaggc tggatgtctt gatcaataac gcagggatct 500
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 aatacggaga catcaatttt gatgacttga acagtgaaca aagctataat 700
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 ttgggtcaaac cactcttcaa tttggtgtca tgggcttttt tcaaaactcc 900
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 acttgttact tgaagaaaaa gaattttgat attggaatag cctgctaaga 1200
 ggtacatgtg ggtatttttg agttactgaa aaattatttt tgggataaga 1250
 gaatttcagc aaagatgttt taaatatata tagtaagtat aatgaataat 1300
 aagtacaatg aaaaatacaa ttatattgta aaattataac tgggcaagca 1350
 tggatgacat attaatatat gtcagaatta agtgactcaa agtgctatcg 1400
 agaggttttt caagtatctt tgagtttcat ggccaaagtg ttaactagtt 1450
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 cacaagtctt acttgaata aatttactgg tac 1533

<210> 303
 <211> 336
 <212> PRT
 <213> Homo sapiens

<400> 303
 Met Ala Val Ala Thr Ala Ala Ala Val Leu Ala Ala Leu Gly Gly
 1 5 10 15
 Ala Leu Trp Leu Ala Ala Arg Arg Phe Val Gly Pro Arg Val Gln
 20 25 30
 Arg Leu Arg Arg Gly Gly Asp Pro Gly Leu Met His Gly Lys Thr
 35 40 45

Val	Leu	Ile	Thr	Gly	Ala	Asn	Ser	Gly	Leu	Gly	Arg	Ala	Thr	Ala	50	55	60
Ala	Glu	Leu	Leu	Arg	Leu	Gly	Ala	Arg	Val	Ile	Met	Gly	Cys	Arg	65	70	75
Asp	Arg	Ala	Arg	Ala	Glu	Glu	Ala	Ala	Gly	Gln	Leu	Arg	Arg	Glu	80	85	90
Leu	Arg	Gln	Ala	Ala	Glu	Cys	Gly	Pro	Glu	Pro	Gly	Val	Ser	Gly	95	100	105
Val	Gly	Glu	Leu	Ile	Val	Arg	Glu	Leu	Asp	Leu	Ala	Ser	Leu	Arg	110	115	120
Ser	Val	Arg	Ala	Phe	Cys	Gln	Glu	Met	Leu	Gln	Glu	Glu	Pro	Arg	125	130	135
Leu	Asp	Val	Leu	Ile	Asn	Asn	Ala	Gly	Ile	Phe	Gln	Cys	Pro	Tyr	140	145	150
Met	Lys	Thr	Glu	Asp	Gly	Phe	Glu	Met	Gln	Phe	Gly	Val	Asn	His	155	160	165
Leu	Gly	His	Phe	Leu	Leu	Thr	Asn	Leu	Leu	Leu	Gly	Leu	Leu	Lys	170	175	180
Ser	Ser	Ala	Pro	Ser	Arg	Ile	Val	Val	Val	Ser	Ser	Lys	Leu	Tyr	185	190	195
Lys	Tyr	Gly	Asp	Ile	Asn	Phe	Asp	Asp	Leu	Asn	Ser	Glu	Gln	Ser	200	205	210
Tyr	Asn	Lys	Ser	Phe	Cys	Tyr	Ser	Arg	Ser	Lys	Leu	Ala	Asn	Ile	215	220	225
Leu	Phe	Thr	Arg	Glu	Leu	Ala	Arg	Arg	Leu	Glu	Gly	Thr	Asn	Val	230	235	240
Thr	Val	Asn	Val	Leu	His	Pro	Gly	Ile	Val	Arg	Thr	Asn	Leu	Gly	245	250	255
Arg	His	Ile	His	Ile	Pro	Leu	Leu	Val	Lys	Pro	Leu	Phe	Asn	Leu	260	265	270
Val	Ser	Trp	Ala	Phe	Phe	Lys	Thr	Pro	Val	Glu	Gly	Ala	Gln	Thr	275	280	285
Ser	Ile	Tyr	Leu	Ala	Ser	Ser	Pro	Glu	Val	Glu	Gly	Val	Ser	Gly	290	295	300
Arg	Tyr	Phe	Gly	Asp	Cys	Lys	Glu	Glu	Glu	Leu	Leu	Pro	Lys	Ala	305	310	315
Met	Asp	Glu	Ser	Val	Ala	Arg	Lys	Leu	Trp	Asp	Ile	Ser	Glu	Val	320	325	330
Met	Val	Gly	Leu	Leu	Lys												

<210> 304
 <211> 521
 <212> DNA
 <213> Homo sapiens

<220>
 <221> unsure
 <222> 20, 34, 62, 87, 221, 229
 <223> unknown base

<400> 304
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 gcaagaaaat tntgggatat cagtgaagtg atggttngcc tgctaaaata 100
 ggaacaagga gtaaaagagc tgtttataaa actgcatatc agttatatct 150
 gtgatcagga atggtgtgga ttgagaactt gttacttgaa gaaaaagaat 200
 tttgatattg gaatagcctg ntaagaggna catgtgggta ttttgagatt 250
 actgaaaaat ttttttggg ataagagaat ttcagcaaag atgttttaaa 300
 tatatatagt aagtataatg aataataagt acaatgaaaa atacaattat 350
 attgtaaaat tataactggg caagcatgga tgacatatta atatttgtca 400
 gaattaagtg actcaaagtg ctatcgagag gtttttcaag tatctttgag 450
 tttcatggcc aaagtgttaa ctagttttac tacaatgttt ggtgtttgtg 500
 tggaaattat ctgcctggct t 521

<210> 305
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 305
 ccaggaaatg ctccaggaag agcc 24

<210> 306
 <211> 26
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 306
 gcccatgaca ccaaattgaa gagtgg 26

<210> 307

<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 307
aacgcaggga tcttccagt cccttacatg aagactgaag atggg 45

<210> 308
<211> 1523
<212> DNA
<213> Homo sapiens

<400> 308
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ccagcgctg tccctgtcac ggaccccagc gttaccatgc atcctgccgt 150
cttctatcc ttacccgacc tcagatgctc ctttctgctc ctggtaactt 200
gggtttttac tctgttaaca actgaaataa caagtcttgc tacagagaat 250
atagatgaaa ttttaaaca tgctgatgtt gctttagtaa atttttatgc 300
tgactggtgt cgtttcagtc agatgttgca tccaattttt gaggaagctt 350
ccgatgtcat taaggaagaa tttccaaatg aaaatcaagt agtgtttgcc 400
agagttgatt gtgatcagca ctctgacata gccagagat acaggataag 450
caaataccca accctcaaat tgtttcgtaa tgggatgatg atgaagagag 500
aatacagggg tcagcgatca gtgaaagcat tggcagatta catcaggcaa 550
caaaaaagtg accccattca agaaattcgg gacttagcag aaatcaccac 600
tcttgatcgc agcaaaagaa atatcattgg atattttgag caaaaggact 650
cggacaacta tagagttttt gaacgagtag cgaatatttt gcatgatgac 700
tgtgcctttc tttctgcatt tggggatgtt tcaaaaccgg aaagatatag 750
tggcgacaac ataatctaca aaccaccagg gcattctgct ccggatatgg 800
tgtacttggg agctatgaca aattttgatg tgacttaca ttggattcaa 850
gataaatgtg ttctcttgt ccgagaaata acatttgaaa atggagagga 900
attgacagaa gaaggactgc cttttctcat actctttcac atgaaagaag 950
atacagaaag tttagaaata ttccagaatg aagtagctcg gcaattaata 1000
agtgaaaaag gtacaataaa ctttttacat gccgattgtg acaaatttag 1050

Tyr	Phe	Glu	Gln	Lys	Asp	Ser	Asp	Asn	Tyr	Arg	Val	Phe	Glu	Arg	170	175	180
Val	Ala	Asn	Ile	Leu	His	Asp	Asp	Cys	Ala	Phe	Leu	Ser	Ala	Phe	185	190	195
Gly	Asp	Val	Ser	Lys	Pro	Glu	Arg	Tyr	Ser	Gly	Asp	Asn	Ile	Ile	200	205	210
Tyr	Lys	Pro	Pro	Gly	His	Ser	Ala	Pro	Asp	Met	Val	Tyr	Leu	Gly	215	220	225
Ala	Met	Thr	Asn	Phe	Asp	Val	Thr	Tyr	Asn	Trp	Ile	Gln	Asp	Lys	230	235	240
Cys	Val	Pro	Leu	Val	Arg	Glu	Ile	Thr	Phe	Glu	Asn	Gly	Glu	Glu	245	250	255
Leu	Thr	Glu	Glu	Gly	Leu	Pro	Phe	Leu	Ile	Leu	Phe	His	Met	Lys	260	265	270
Glu	Asp	Thr	Glu	Ser	Leu	Glu	Ile	Phe	Gln	Asn	Glu	Val	Ala	Arg	275	280	285
Gln	Leu	Ile	Ser	Glu	Lys	Gly	Thr	Ile	Asn	Phe	Leu	His	Ala	Asp	290	295	300
Cys	Asp	Lys	Phe	Arg	His	Pro	Leu	Leu	His	Ile	Gln	Lys	Thr	Pro	305	310	315
Ala	Asp	Cys	Pro	Val	Ile	Ala	Ile	Asp	Ser	Phe	Arg	His	Met	Tyr	320	325	330
Val	Phe	Gly	Asp	Phe	Lys	Asp	Val	Leu	Ile	Pro	Gly	Lys	Leu	Lys	335	340	345
Gln	Phe	Val	Phe	Asp	Leu	His	Ser	Gly	Lys	Leu	His	Arg	Glu	Phe	350	355	360
His	His	Gly	Pro	Asp	Pro	Thr	Asp	Thr	Ala	Pro	Gly	Glu	Gln	Ala	365	370	375
Gln	Asp	Val	Ala	Ser	Ser	Pro	Pro	Glu	Ser	Ser	Phe	Gln	Lys	Leu	380	385	390
Ala	Pro	Ser	Glu	Tyr	Arg	Tyr	Thr	Leu	Leu	Arg	Asp	Arg	Asp	Glu	395	400	405

Leu

<210> 310
 <211> 182
 <212> DNA
 <213> Homo sapiens

<220>
 <221> unsure

<222> 36, 48
<223> unknown base

<400> 310
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ttgtgatcag cactctgaca tagcccagag atacaggata agcaaatacc 100
caaccctcaa attgtttcgt aatgggatga tgatgaagag agaatacagg 150
ggtcagcgat cagtgaagc attggcagat ta 182

<210> 311
<211> 598
<212> DNA
<213> Homo sapiens

<220>
<221> unsure
<222> 38, 59, 140, 169, 174, 183, 282-283, 294-295, 319, 396
<223> unknown base

<400> 311
agaggcctct ctggaagttg tcccgggtgt tcgccgcngg agcccgggtc 50
gagaggacna ggtgccgctg cctggagaat cctccgctgc cgtcggctcc 100
cggagcccag ccctttccta acccaaccca acctagcccn gtcccagccg 150
ccagcgcttg tccctgtcnc ggancccagc gtnaccatgc atcctgccgt 200
cttcctatcc ttaccgagcc tcagatgctc cttctgctc ctggtaactt 250
gggtttttac tcctgtaaca actgaaataa cnngtcttga tacnnagaat 300
atagatgaaa ttttaaacna tgctgatgtg gctttagtca atttttatgc 350
tgactggtgt cgtttcagtc agatgtggca tccaattttt gaggangctt 400
ccgatgtcat taaggaagaa tttccaaatg aaaatcaagt agtgtttgcc 450
agagttgatt gtgatcagca ctctgacata gccagagat acaggataag 500
caaataccca accctcaaat tgtttcgtaa tgggatgatg atgaagagag 550
aatacagggg tcagcgatca gtgaaagcat tggcagatta catcaggc 598

<210> 312
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 312
tgagaggcct ctctggaagt tg 22

<210> 313
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 313
gtcagcgatc agtgaaagc 19

<210> 314
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 314
ccagaatgaa gtagctcggc 20

<210> 315
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 315
ccgactcaaa atgcattgtc 20

<210> 316
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 316
catttggcag gaattgtcc 19

<210> 317
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 317
ggtgctatag gccaaagg 18

<210> 318
<211> 24
<212> DNA

Variable	Mean	Standard Deviation	Minimum	Maximum
Age	34.5	10.2	22	55
Gender	0.5	0.5	0	1
Marital Status	0.7	0.5	0	1
Education	12.5	1.5	10	15
Income	3500	1500	1000	7000
Health	0.8	0.3	0	1
Stress	4.5	1.5	1	7
Depression	0.2	0.4	0	1
Life Satisfaction	5.5	1.5	1	9
Resilience	6.5	1.5	1	9
Optimism	7.5	1.5	1	9
Gratitude	8.5	1.5	1	9
Forgiveness	7.5	1.5	1	9
Compassion	8.5	1.5	1	9
Kindness	8.5	1.5	1	9
Generosity	8.5	1.5	1	9
Patience	8.5	1.5	1	9
Humility	8.5	1.5	1	9
Modesty	8.5	1.5	1	9
Self-control	8.5	1.5	1	9
Discipline	8.5	1.5	1	9
Perseverance	8.5	1.5	1	9
Endurance	8.5	1.5	1	9
Stamina	8.5	1.5	1	9
Strength	8.5	1.5	1	9
Power	8.5	1.5	1	9
Influence	8.5	1.5	1	9
Authority	8.5	1.5	1	9
Leadership	8.5	1.5	1	9
Management	8.5	1.5	1	9
Organization	8.5	1.5	1	9
Planning	8.5	1.5	1	9
Execution	8.5	1.5	1	9
Completion	8.5	1.5	1	9
Success	8.5	1.5	1	9
Accomplishment	8.5	1.5	1	9
Achievement	8.5	1.5	1	9
Realization	8.5	1.5	1	9
Fulfillment	8.5	1.5	1	9
Satisfaction	8.5	1.5	1	9
Contentment	8.5	1.5	1	9
Peace	8.5	1.5	1	9
Harmony	8.5	1.5	1	9
Balance	8.5	1.5	1	9
Stability	8.5	1.5	1	9
Consistency	8.5	1.5	1	9
Reliability	8.5	1.5	1	9
Trustworthiness	8.5	1.5	1	9
Honesty	8.5	1.5	1	9
Integrity	8.5	1.5	1	9
Authenticity	8.5	1.5	1	9
Genuineness	8.5	1.5	1	9
Sincerity	8.5	1.5	1	9
Openness	8.5	1.5	1	9
Transparency	8.5	1.5	1	9
Communication	8.5	1.5	1	9
Expression	8.5	1.5	1	9
Interaction	8.5	1.5	1	9
Relationship	8.5	1.5	1	9
Connection	8.5	1.5	1	9
Engagement	8.5	1.5	1	9
Participation	8.5	1.5	1	9
Involvement	8.5	1.5	1	9
Contribution	8.5	1.5	1	9
Service	8.5	1.5	1	9
Helpfulness	8.5	1.5	1	9
Usefulness	8.5	1.5	1	9
Value	8.5	1.5	1	9
Importance	8.5	1.5	1	9
Significance	8.5	1.5	1	9
Meaning	8.5	1.5	1	9
Purpose	8.5	1.5	1	9
Goal	8.5	1.5	1	9
Direction	8.5	1.5	1	9
Focus	8.5	1.5	1	9
Attention	8.5	1.5	1	9
Interest	8.5	1.5	1	9
Curiosity	8.5	1.5	1	9
Wonder	8.5	1.5	1	9
Admiration	8.5	1.5	1	9
Appreciation	8.5	1.5	1	9
Gratitude	8.5	1.5	1	9
Thankfulness	8.5	1.5	1	9
Recognition	8.5	1.5	1	9
Acknowledgment	8.5	1.5	1	9
Validation	8.5	1.5	1	9

<223> Synthetic oligonucleotide probe

ctgtatctct gggctatgtc agag 24

<211> 25

<213> Artificial Sequence

<223> Synthetic oligonucleotide probe

ctacatataa tggcacatgt cagcc 25

<211> 46

<213> Artificial Sequence

<223> Synthetic oligonucleotide probe

cgtcttccta tccttaccgc acctcagatg ctcccttctg ctccctg 46

<211> 1333

<213> Homo sapiens

gcccacgcgt	ccgatggcgt	tcacgttcgc	ggccttctgc	tacatgctgg	50
cgctgctgct	cactgccgcg	ctcatcttct	tggccatttg	gcacattata	100
gcatttgatg	agctgaagac	tgattacaag	aatcctatag	accagtgtaa	150
tacctgaat	ccccttgtag	tcccagagta	cctcatccac	gctttcttct	200
gtgtcatgtt	tctttgtgca	gcagagtggc	ttacactggg	tctcaatatg	250
cccctcttgg	catatcatat	ttggaggtat	atgagtagac	cagtgatgag	300
tggccagga	ctctatgacc	ctacaaccat	catgaatgca	gatattctag	350
catattgtca	gaagggaagga	tgggtgcaaat	tagcttttta	tcttctagca	400
tttttttact	acctatatgg	catgatctat	gttttggtga	gctcttagaa	450
caacacacag	aagaatttgt	ccagttaagt	gcattgcaaaa	agccacaaaa	500
tgaagggatt	ctatccagca	agatcctgtc	caagagttagc	ctgtggaatc	550

tgatcagtta ctttaaaaaa tgactcctta ttttttaa at gtttccacat 600
 ttttgcttgt ggaaagactg ttttcatatg ttatactcag ataaagattt 650
 taaatgggtat tacgtataaa ttaatatata atgattacot ctgggtgttga 700
 cagggttgaa ctgactcttc ttaaggaaca gccataatcc tctgaatgat 750
 gcattaatta ctgactgtcc tagtacattg gaagcttttg tttataggaa 800
 cttgtagggc tcatttttgg ttcattgaaa cagtatctaa ttataaatta 850
 gctgtagata tcagggtgctt ctgatgaagt gaaaatgtat atctgactag 900
 tgggaaaactt catgggtttc ctcatctgtc atgtcgatga ttatatatgg 950
 atacatttac aaaaataaaa agcgggaatt ttcccttcgc ttgaatatta 1000
 tccctgtata ttgcatgaat gagagatttc ccatatttcc atcagagtaa 1050
 taaatatact tgctttaatt cttaagcata agtaaacaatg atataaaaaat 1100
 atatgctgaa ttacttgtga agaatgcatt taaagctatt ttaaagtgtg 1150
 ttttatttgt aagacattac ttattaagaa attggttatt atgcttactg 1200
 ttctaactctg gtggttaaagg tattcttaag aatttgcagg tactacagat 1250
 tttcaaaaact gaatgagaga aaattgtata accatcctgc tgttccttta 1300
 gtgcaataca ataaaactct gaaattaaga ctc 1333

<210> 322
 <211> 144
 <212> PRT
 <213> Homo sapiens

<400> 322
 Met Ala Phe Thr Phe Ala Ala Phe Cys Tyr Met Leu Ala Leu Leu
 1 5 10 15
 Leu Thr Ala Ala Leu Ile Phe Phe Ala Ile Trp His Ile Ile Ala
 20 25 30
 Phe Asp Glu Leu Lys Thr Asp Tyr Lys Asn Pro Ile Asp Gln Cys
 35 40 45
 Asn Thr Leu Asn Pro Leu Val Leu Pro Glu Tyr Leu Ile His Ala
 50 55 60
 Phe Phe Cys Val Met Phe Leu Cys Ala Ala Glu Trp Leu Thr Leu
 65 70 75
 Gly Leu Asn Met Pro Leu Leu Ala Tyr His Ile Trp Arg Tyr Met
 80 85 90
 Ser Arg Pro Val Met Ser Gly Pro Gly Leu Tyr Asp Pro Thr Thr
 95 100 105

Ile	Met	Asn	Ala	Asp	Ile	Leu	Ala	Tyr	Cys	Gln	Lys	Glu	Gly	Trp
				110					115					120
Cys	Lys	Leu	Ala	Phe	Tyr	Leu	Leu	Ala	Phe	Phe	Tyr	Tyr	Leu	Tyr
				125					130					135
Gly	Met	Ile	Tyr	Val	Leu	Val	Ser	Ser						
				140										

<210> 323
 <211> 477
 <212> DNA
 <213> Homo sapiens

<400> 323
 attatagcat ttgatgagct gaagactgat tacaagatcc tatagaccag 50
 tgtaataccc tgaatcccct tgtactccca gagtaccta tccacgcttt 100
 cttctgtgtc atgtttcttt gtgcagcaga gtggcttaca ctgggtctca 150
 atatgcccct cttggcatat catatttga ggtatatgag tagaccagt 200
 atgagtggcc caggactcta tgaccctaca accatcatga atgcagatat 250
 tctagcatat tgtcagaagg aaggatgggtg caaattagct ttttatcttc 300
 tagcattttt ttactaccta tatggcatga tctatgtttt ggtgagctct 350
 tagaacaaca cacagaagaa ttggtccagt taagtgcag caaaaagcca 400
 ccaaatgaag ggattctatc cagcaagatc ctgtccaaga gtagcctgtg 450
 gaatctgatc agttacttta aaaaatg 477

<210> 324
 <211> 43
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 324
 tgtaaaacga cggccagtta aatagacctg caattattaa tct 43

<210> 325
 <211> 41
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 325
 caggaaacag ctatgaccac ctgcacacct gcaaattccat t 41

<210> 326

<211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 326
 gtgcagcaga gtggcttaca 20

<210> 327
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 327
 actggaccaa ttcttctgtg 20

<210> 328
 <211> 45
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 328
 gatattctag catattgtca gaaggaagga tgggtcaaat tagct 45

<210> 329
 <211> 1174
 <212> DNA
 <213> Homo sapiens

<400> 329
 cggacgcgtg ggggaaaccc ttccgagaaa acagcaacaa gctgagctgc 50
 tgtgacagag gggaacaaga tggcggcgcc gaaggggagc ctctgggtga 100
 ggacccaact ggggctcccg ccgctgctgc tgctgaccat ggccttggcc 150
 ggaggttcgg ggaccgcttc ggctgaagca tttgactcgg tcttgggtga 200
 tacggcgtct tgccaccggg cctgtcagtt gacctacccc ttgcacacct 250
 accctaagga agaggagttg tacgcatgtc agagaggttg caggctgttt 300
 tcaatttgtc agtttgtgga tgatggaatt gacttaaadc gaactaaatt 350
 ggaatgtgaa tctgcatgta cagaagcata ttcccaatct gatgagcaat 400
 atgcttgcca tcttggttgc cagaatcagc tgccattcgc tgaactgaga 450
 caagaacaac ttatgtccct gatgccaaaa atgcacctac tctttcctct 500

aactctggtg aggtcattct ggagtgcacat gatggactcc gcacagagct 550
tcataacctc ttcattggact ttttatcttc aagccgatga cggaaaaata 600
gttatattcc agtctaagcc agaaatccag tacgcaccac atttgagca 650
ggagcctaca aatttgagag aatcatctct aagcaaatg tcctatctgc 700
aaatgagaaa ttcacaagcg cacaggaatt ttcttgaaga tggagaaagt 750
gatggctttt taagatgcct ctctcttaac tctgggtgga ttttaactac 800
aactcttgtc ctctcgggtga tggatttgc ttggatttgc tgtgcaactg 850
ttgctacagc tgtggagcag tatgttccct ctgagaagct gagtatctat 900
gggtgacttg agtttatgaa tgaacaaaag ctaaacagat atccagcttc 950
ttctcttggt gttgttagat ctaaaactga agatcatgaa gaagcagggc 1000
ctctacctac aaaagtgaat cttgctcatt ctgaaattta agcatttttc 1050
ttttaaaaga caagtgaat agacatctaa aattccactc ctcatagagc 1100
ttttaaaatg gtttcattgg atataggcct taagaaatca ctataaaatg 1150
caaataaagt tactcaaatc tgtg 1174

<210> 330
<211> 323
<212> PRT
<213> Homo sapiens

<400> 330
Met Ala Ala Pro Lys Gly Ser Leu Trp Val Arg Thr Gln Leu Gly
1 5 10 15
Leu Pro Pro Leu Leu Leu Leu Thr Met Ala Leu Ala Gly Gly Ser
20 25 30
Gly Thr Ala Ser Ala Glu Ala Phe Asp Ser Val Leu Gly Asp Thr
35 40 45
Ala Ser Cys His Arg Ala Cys Gln Leu Thr Tyr Pro Leu His Thr
50 55 60
Tyr Pro Lys Glu Glu Glu Leu Tyr Ala Cys Gln Arg Gly Cys Arg
65 70 75
Leu Phe Ser Ile Cys Gln Phe Val Asp Asp Gly Ile Asp Leu Asn
80 85 90
Arg Thr Lys Leu Glu Cys Glu Ser Ala Cys Thr Glu Ala Tyr Ser
95 100 105
Gln Ser Asp Glu Gln Tyr Ala Cys His Leu Gly Cys Gln Asn Gln
110 115 120

Leu	Pro	Phe	Ala	Glu 125	Leu	Arg	Gln	Glu	Gln 130	Leu	Met	Ser	Leu	Met 135
Pro	Lys	Met	His	Leu 140	Leu	Phe	Pro	Leu	Thr 145	Leu	Val	Arg	Ser	Phe 150
Trp	Ser	Asp	Met	Met 155	Asp	Ser	Ala	Gln	Ser 160	Phe	Ile	Thr	Ser	Ser 165
Trp	Thr	Phe	Tyr	Leu 170	Gln	Ala	Asp	Asp	Gly 175	Lys	Ile	Val	Ile	Phe 180
Gln	Ser	Lys	Pro	Glu 185	Ile	Gln	Tyr	Ala	Pro 190	His	Leu	Glu	Gln	Glu 195
Pro	Thr	Asn	Leu	Arg 200	Glu	Ser	Ser	Leu	Ser 205	Lys	Met	Ser	Tyr	Leu 210
Gln	Met	Arg	Asn	Ser 215	Gln	Ala	His	Arg	Asn 220	Phe	Leu	Glu	Asp	Gly 225
Glu	Ser	Asp	Gly	Phe 230	Leu	Arg	Cys	Leu	Ser 235	Leu	Asn	Ser	Gly	Trp 240
Ile	Leu	Thr	Thr	Thr 245	Leu	Val	Leu	Ser	Val 250	Met	Val	Leu	Leu	Trp 255
Ile	Cys	Cys	Ala	Thr 260	Val	Ala	Thr	Ala	Val 265	Glu	Gln	Tyr	Val	Pro 270
Ser	Glu	Lys	Leu	Ser 275	Ile	Tyr	Gly	Asp	Leu 280	Glu	Phe	Met	Asn	Glu 285
Gln	Lys	Leu	Asn	Arg 290	Tyr	Pro	Ala	Ser	Ser 295	Leu	Val	Val	Val	Arg 300
Ser	Lys	Thr	Glu	Asp 305	His	Glu	Glu	Ala	Gly 310	Pro	Leu	Pro	Thr	Lys 315
Val	Asn	Leu	Ala	His 320	Ser	Glu	Ile							

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<210> 331
<211> 350
<212> DNA
<213> Homo sapiens
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<400> 331
ttgggtgata cggcgtcttg ccaccgggcc tgtcagttga cctaccctt 50
gcacacctac cctaaggaag aggagttgta cgcattgcag agaggttgca 100
ggctgttttc aatttgtcag tttgtggatg atggaattga cttaaattga 150
actaaattgg aatgtgaatc tgcattgaca gaagcatatt cccaattctga 200
tgagcaatat gcttgccatc ttggttgcca gaatcagctg ccattcgtctg 250
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aactgagaca agaacaactt atgtccctga tgccaaaaat gcacctactc 300
 ttctctctaa ctctggtgag gtcattctgg agtgacatga tggactccgc 350

<210> 332
 <211> 562
 <212> DNA
 <213> Homo sapiens

<220>
 <221> unsure
 <222> 47
 <223> unknown base

<400> 332
 cacactggcc ggatctttta gagtcctttg accttgacca agggtcngga 50
 aaacagcaac aagctgagct gctgtgacag agggacaag atggcggcgc 100
 cgaagggagc ctttggtgga ggaccaact ggggctcccg ccgctgctgc 150
 tgctgaccat ggccttggcc ggaggttcgg ggaccgcttc ggctgaagca 200
 ttgactcgg tcttggtgga tacggcgtct tgccaccggg cctgtcagtt 250
 gacctacccc ttgcacacct accctaagga agaggagttg tacgcatgtc 300
 agagaggttg caggctgttt tcaatttgct agtttggtga tgatggaatt 350
 gacttaaata gaactaaatt ggaatgtgaa tctgcatgta cagaagcata 400
 ttcccaatct gatgagcaat atgcttgcca tcttggttgc cagaatcagc 450
 tgccattcgc tgaactgaga caagaacaac ttatgtccct gatgccaaaa 500
 atgcacctac tctttcctct aactctggtg aggtcattct ggagtgacat 550
 gatggactcc gc 562

<210> 333
 <211> 22
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 333
 acaagctgag ctgctgtgac ag 22

<210> 334
 <211> 22
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 334
tgattctggc aaccaagatg gc 22

<210> 335

<211> 40

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 335

atggccttgg ccggagggtc ggggaccgct tcggctgaag 40

<210> 336

<211> 1885

<212> DNA

<213> Homo sapiens

<400> 336

gcgagggtggc gatcgctgag aggcaggagg gccgaggcgg gcctggggagg 50

cgggcccgag gtggggcgcc gctggggccg gcccgcacgg gcttcatctg 100

agggcgacag gcccgcgacc gagcgtgcgg actggcctcc caagcgtggg 150

gcgacaagct gccggagctg caatgggccg cggctgggga ttcttgtttg 200

gcctcctggg cgccgtgtgg ctgctcagct cgggccacgg agaggagcag 250

cccccgaga cagcggcaca gaggtgcttc tgccaggtta gtggttactt 300

ggatgattgt acctgtgatg ttgaaaccat tgatagattt aataactaca 350

ggcttttccc aagactacaa aaacttcttg aaagtgacta ctttaggtat 400

tacaaggtaa acctgaagag gccgtgtcct ttctggaatg acatcagcca 450

gtgtggaaga agggactgtg ctgtcaaacc atgtcaatct gatgaagttc 500

ctgatggaat taaatctgag agctacaagt attctgaaga agccaataat 550

ctcattgaag aatgtgaaca agctgaacga cttggagcag tggatgaatc 600

tctgagttag gaaacacaga aggctgttct tcagtggacc aagcatgatg 650

attcttcaga taactttctg gaagctgatg acattcagtc ccctgaagct 700

gaatatgtag atttgcttct taatcctgag cgctacactg gttacaaggg 750

accagatgct tggaaaatat ggaatgtcat ctacgaagaa aactgtttta 800

agccacagac aattaaaaga cttttaaatc ctttggcttc tgggtcaaggg 850

acaagtgaag agaacacttt ttacagttgg ctagaaggtc tctgtgtaga 900

aaaaagagca ttctacagac ttatatctgg cctacatgca agcattaatg 950

Tyr	Tyr	Lys	Val	Asn	Leu	Lys	Arg	Pro	Cys	Pro	Phe	Trp	Asn	Asp	
				80					85					90	
Ile	Ser	Gln	Cys	Gly	Arg	Arg	Asp	Cys	Ala	Val	Lys	Pro	Cys	Gln	
				95					100					105	
Ser	Asp	Glu	Val	Pro	Asp	Gly	Ile	Lys	Ser	Ala	Ser	Tyr	Lys	Tyr	
				110					115					120	
Ser	Glu	Glu	Ala	Asn	Asn	Leu	Ile	Glu	Glu	Cys	Glu	Gln	Ala	Glu	
				125					130					135	
Arg	Leu	Gly	Ala	Val	Asp	Glu	Ser	Leu	Ser	Glu	Glu	Thr	Gln	Lys	
				140					145					150	
Ala	Val	Leu	Gln	Trp	Thr	Lys	His	Asp	Asp	Ser	Ser	Asp	Asn	Phe	
				155					160					165	
Cys	Glu	Ala	Asp	Asp	Ile	Gln	Ser	Pro	Glu	Ala	Glu	Tyr	Val	Asp	
				170					175					180	
Leu	Leu	Leu	Asn	Pro	Glu	Arg	Tyr	Thr	Gly	Tyr	Lys	Gly	Pro	Asp	
				185					190					195	
Ala	Trp	Lys	Ile	Trp	Asn	Val	Ile	Tyr	Glu	Glu	Asn	Cys	Phe	Lys	
				200					205					210	
Pro	Gln	Thr	Ile	Lys	Arg	Pro	Leu	Asn	Pro	Leu	Ala	Ser	Gly	Gln	
				215					220					225	
Gly	Thr	Ser	Glu	Glu	Asn	Thr	Phe	Tyr	Ser	Trp	Leu	Glu	Gly	Leu	
				230					235					240	
Cys	Val	Glu	Lys	Arg	Ala	Phe	Tyr	Arg	Leu	Ile	Ser	Gly	Leu	His	
				245					250					255	
Ala	Ser	Ile	Asn	Val	His	Leu	Ser	Ala	Arg	Tyr	Leu	Leu	Gln	Glu	
				260					265					270	
Thr	Trp	Leu	Glu	Lys	Lys	Trp	Gly	His	Asn	Ile	Thr	Glu	Phe	Gln	
				275					280					285	
Gln	Arg	Phe	Asp	Gly	Ile	Leu	Thr	Glu	Gly	Glu	Gly	Pro	Arg	Arg	
				290					295					300	
Leu	Lys	Asn	Leu	Tyr	Phe	Leu	Tyr	Leu	Ile	Glu	Leu	Arg	Ala	Leu	
				305					310					315	
Ser	Lys	Val	Leu	Pro	Phe	Phe	Glu	Arg	Pro	Asp	Phe	Gln	Leu	Phe	
				320					325					330	
Thr	Gly	Asn	Lys	Ile	Gln	Asp	Glu	Glu	Asn	Lys	Met	Leu	Leu	Leu	
				335					340					345	
Glu	Ile	Leu	His	Glu	Ile	Lys	Ser	Phe	Pro	Leu	His	Phe	Asp	Glu	
				350					355					360	
Asn	Ser	Phe	Phe	Ala	Gly	Asp	Lys	Lys	Glu	Ala	His	Lys	Leu	Lys	

365	370	375
Glu Asp Phe Arg Leu His Phe Arg Asn Ile Ser Arg Ile Met Asp		
380	385	390
Cys Val Gly Cys Phe Lys Cys Arg Leu Trp Gly Lys Leu Gln Thr		
395	400	405
Gln Gly Leu Gly Thr Ala Leu Lys Ile Leu Phe Ser Glu Lys Leu		
410	415	420
Ile Ala Asn Met Pro Glu Ser Gly Pro Ser Tyr Glu Phe His Leu		
425	430	435
Thr Arg Gln Glu Ile Val Ser Leu Phe Asn Ala Phe Gly Arg Ile		
440	445	450
Ser Thr Ser Val Lys Glu Leu Glu Asn Phe Arg Asn Leu Leu Gln		
455	460	465
Asn Ile His		

<210> 338
 <211> 507
 <212> DNA
 <213> Homo sapiens

<220>
 <221> unsure
 <222> 101, 263, 376, 397, 426
 <223> unknown base

<400> 338
 gctggaaata tggatgtcat ctacgagaaa ctgttttaag ccacagacaa 50
 ttaaaagacc tttaaactct ttggcttctg gtcaagggac aagtgaagag 100
 nacacttttt acagttggct agaaggtctc tgtgtagaaa aaagagcatt 150
 ctacagactt atatctggcc tacatgcaag cattaatgtg ctttgagtg 200
 caagatatct ttacaagag acctgggttag aaaagaaatg gggacacaac 250
 attacagaat ttnaacagcg atttgatgga attttgactg aaggagaagg 300
 tccaagaagg ctaagaact tgtattttct ctacttaata gaactaagg 350
 ctttatccaa agtggtacca ttcttngagc gccagattt tcaactnttt 400
 actggaaata aaattcagga tgaggnaaac aaaatgttac ttttgaaat 450
 acttcatgaa atcaagtcatt ttcttttgca ttttgatgag aattcatttt 500
 tttgctg 507

<210> 339
 <211> 20

<220>

<223> Synthetic oligonucleotide probe

<400> 344

agacagcggc acagaggtgc ttctgccagg ttagtggtta cttggatgat 50

<210> 345

<211> 1486

<212> DNA

<213> Homo sapiens

<400> 345

cggacgcgtg ggcggacgcg tggcgacgcg cgtgggttgg gagggggcag 50
gatgggaggg aaagtgaaga aaacagaaaa ggagagggac agaggccaga 100
ggactttctca tactggacag aaaccgatca ggcatggaac tccccctcgt 150
cactcacctg ttcttgcccc tgggtgttct gacaggtctc tgctccccct 200
ttaacctgga tgaacatcac ccacgcctat tcccagggcc accagaagct 250
gaatttgat acagtgtctt acaacatgtt gggggtggac agcgatggat 300
gctggtgggc gccccctggg atgggccttc aggcgaccgg aggggggacg 350
tttatcgctg ccctgtaggg ggggccaca atgccccatg tgccaagggc 400
cacttaggtg actaccaact gggaaattca tctcatctg ctgtgaatat 450
gcacctgggg atgtctctgt tagagacaga tggatgatgg ggattcatgg 500
tgagctaagg agagggtggg ggcagtgtct ctgaaggctc ataaaagaaa 550
aaagagaagt gtggtgaagg aaaatggtct gtgtggaggg gtcaaggagt 600
taaaaaccct agaaagcaaa aggtaggtaa tgtcaggag tagtcttcat 650
gcctccttca actgggagca tgttctgagg gtgccctccc aagcctggga 700
gtaactattt ccccatccc caggcctgtg cccctctctg gtctctgtgt 750
tgtggcagct ctgtcttcag ttctgggata tgtgcccgtg tggatgcttc 800
attccagcct cagggaagcc tggcaccac tgccaacgt gagccagagg 850
aaggctgagt acttggttcc cagaaggaga tactgggtgg gaaaaagatg 900
gggcaaagcg gtatgatgcc tggcaaaggg cctgcatggc taccctcatt 950
gctaccta atgtgcttgcaa aagctccatg tttcctaaca gattcagact 1000
cctggccagg tgtggtggcc cacacctgta attctagcac tttgggaggc 1050
caaggtgggc agatcacttg aggtcaggag ttcaagacca gcctggccaa 1100
catggtgaaa ctccatctct actaaaaaaaa aaaaaataca aaaattagct 1150

gggtgcgcta gtgcatgcct gtaatctcat ctactcggga ggctaagaca 1200
 ggagactctc acttcaaccc aggaggtgga ggttgcggtg agccaagatt 1250
 gtgcctctgc actctagcgt gggtgacaga gtaagcgaga ctccatctca 1300
 aaaataataa taataataat tcagactcct tatcaggagt ccatgatctg 1350
 gcctggcaca gtaactcatg cctgtaatcc caacattttg ggaggccaac 1400
 gcaggaggat tgcttgaggt ctggaggttt gagaccagcc tgggcaacat 1450
 agaagagccc catctctaaa taaatgtttt aaaaat 1486

<210> 346
 <211> 124
 <212> PRT
 <213> Homo sapiens

<400> 346
 Met Glu Leu Pro Phe Val Thr His Leu Phe Leu Pro Leu Val Phe
 1 5 10 15
 Leu Thr Gly Leu Cys Ser Pro Phe Asn Leu Asp Glu His His Pro
 20 25 30
 Arg Leu Phe Pro Gly Pro Pro Glu Ala Glu Phe Gly Tyr Ser Val
 35 40 45
 Leu Gln His Val Gly Gly Gly Gln Arg Trp Met Leu Val Gly Ala
 50 55 60
 Pro Trp Asp Gly Pro Ser Gly Asp Arg Arg Gly Asp Val Tyr Arg
 65 70 75
 Cys Pro Val Gly Gly Ala His Asn Ala Pro Cys Ala Lys Gly His
 80 85 90
 Leu Gly Asp Tyr Gln Leu Gly Asn Ser Ser His Pro Ala Val Asn
 95 100 105
 Met His Leu Gly Met Ser Leu Leu Glu Thr Asp Gly Asp Gly Gly
 110 115 120
 Phe Met Val Ser

<210> 347
 <211> 509
 <212> DNA
 <213> Homo sapiens

<220>
 <221> unsure
 <222> 22
 <223> unknown base

<400> 347

cacagttccc caccatcaact cntcccatte cttccaactt tatttttagc 50
 ttgccattgg gagggggcag gatgggaggg aaagtgaaga aaacagaaaa 100
 ggagaggggac agaggccaga ggactttctca tactggacag aaaccgatca 150
 ggcatggaac tccccttctg cactcacctg ttcttgcccc tgggtgttcct 200
 gacagggtctc tgctccccct ttaacctgga tgaacatcac ccacgcctat 250
 tcccagggcc accagaagct gaatttggat acagtgtctt acaacatggt 300
 ggggggtggac agcgatggat gctggtgggc gccccctggg atgggccttc 350
 aggcgaccgg aggggggacg tttatcgctg ccctgtaggg ggggcccaca 400
 atgccccatg tgccaagggc cacttaggtg actaccaact gggaaattca 450
 tctcatcctg ctgtgaatat gcacctgggg atgtctctgt tagagacaga 500
 tggatgatgg 509

<210> 348
 <211> 23
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 348
 agggacagag gccagaggac ttc 23

<210> 349
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 349
 caggtgcata ttcacagcag gatg 24

<210> 350
 <211> 45
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 350
 ggaactcccc ttcgtcactc acctgttctt gccccctggtg ttctct 45

<210> 351
 <211> 2056
 <212> DNA

<213> Homo sapiens

<400> 351

aaagttacat tttctctgga actctcctag gccactccct gctgatgcaa 50
catctgggtt tgggcagaaa ggagggtgct tcggagcccg ccctttctga 100
gcttcctggg ccggctctag aacaattcag gcttcgctgc gactcagacc 150
tcagctccaa catatgcatt ctgaagaaag atggctgaga tggacagaat 200
gctttatttt ggaaagaaac aatgttctag gtcaaactga gtctacaaa 250
tgcagacttt cacaatgggt ctagaagaaa tctggacaag tcttttcatg 300
tggtttttct acgcattgat tccatgtttg ctcacagatg aagtggccat 350
tctgcctgcc cctcagaacc tctctgtact ctcaaccaac atgaagcatc 400
tcttgatgtg gagcccagtg atcgcgcctg gagaaacagt gtactattct 450
gtcgaatacc agggggagta cgagagcctg tacacgagcc acatctggat 500
ccccagcagc tgggtgtcac tcaactgaagg tcctgagtgt gatgtcactg 550
atgacatcac ggccactgtg ccatacaacc ttcgtgtcag ggccacattg 600
gggtcacaga cctcagcctg gagcatcctg aagcatccct ttaatagaaa 650
ctcaaccatc cttacccgac ctgggatgga gatcacaaa gatggcttcc 700
acctggttat ttagctggag gacctggggc ccagtttga gttccttgtg 750
gcctactgga ggaggagcc tgggtgccgag gaacatgtca aaatggtgag 800
gagtgggggt attccagtgc acctagaaac catggagcca ggggctgcat 850
actgtgtgaa ggcccagaca ttcgtgaagg ccattgggag gtacagcgcc 900
ttcagccaga cagaatgtgt ggagggtgcaa ggagaggcca ttcccctggt 950
actggccctg tttgctttg ttggcttcat gctgatcctt gtggtcgtgc 1000
cactgttcgt ctggaaaatg ggccggctgc tccagtactc ctgttgcccc 1050
gtggtggtcc tcccagacac cttgaaaata accaattcac ccagaagtt 1100
aatcagctgc agaaggagg aggtggatgc ctgtgccacg gctgtgatgt 1150
ctcctgagga actcctcagg gcctggatct cataggtttg cggaagggcc 1200
cagggtgaagc cgagaacctg gtctgcatga catggaaacc atgaggggac 1250
aagttgtgtt tctgttttcc gccacggaca agggatgaga gaagtaggaa 1300
gagcctgttg tctacaagtc tagaagcaac catcagaggc agggtggttt 1350
gtctaacaga aactgactg aggcttaggg gatgtgacct ctagactggg 1400

ggctgccact tgctggctga gcaaccctgg gaaaagtgc ttcacccctt 1450
 cggtcctaag ttttctcadc tgtaatgggg gaattaccta cacacctgct 1500
 aaacacacac acacagagtc tctctctata tatacacacg tacacataaa 1550
 tacacccagc acttgcaagg ctagagggaa actggtgaca ctctacagtc 1600
 tgactgattc agtgtttctg gagagcagga cataaatgta tgatgagaat 1650
 gatcaaggac tctacacact ggggtggcttg gagagcccac tttcccagaa 1700
 taatccttga gagaaaagga atcatgggag caatggtgtt gagttcactt 1750
 caagcccaat gccggtgcag aggggaatgg cttagcgagc tctacagtag 1800
 gtgacctgga ggaaggtcac agccacactg aaaatgggat gtgcatgaac 1850
 acggaggatc catgaactac tgtaaagtgt tgacagtgtg tgcacactgc 1900
 agacagcagg tgaaatgtat gtgtgcaatg cgacgagaat gcagaagtca 1950
 gtaacatgtg catgtttgtt gtgctccttt tttctgttgg taaagtacag 2000
 aattcagcaa ataaaaaggg ccaccctggc caaaagcggg aaaaaaaaaa 2050
 aaaaaa 2056

<210> 352
 <211> 311
 <212> PRT
 <213> Homo sapiens

<400> 352
 Met Gln Thr Phe Thr Met Val Leu Glu Glu Ile Trp Thr Ser Leu
 1 5 10 15
 Phe Met Trp Phe Phe Tyr Ala Leu Ile Pro Cys Leu Leu Thr Asp
 20 25 30
 Glu Val Ala Ile Leu Pro Ala Pro Gln Asn Leu Ser Val Leu Ser
 35 40 45
 Thr Asn Met Lys His Leu Leu Met Trp Ser Pro Val Ile Ala Pro
 50 55 60
 Gly Glu Thr Val Tyr Tyr Ser Val Glu Tyr Gln Gly Glu Tyr Glu
 65 70 75
 Ser Leu Tyr Thr Ser His Ile Trp Ile Pro Ser Ser Trp Cys Ser
 80 85 90
 Leu Thr Glu Gly Pro Glu Cys Asp Val Thr Asp Asp Ile Thr Ala
 95 100 105
 Thr Val Pro Tyr Asn Leu Arg Val Arg Ala Thr Leu Gly Ser Gln
 110 115 120

Thr	Ser	Ala	Trp	Ser	Ile	Leu	Lys	His	Pro	Phe	Asn	Arg	Asn	Ser	
				125					130					135	
Thr	Ile	Leu	Thr	Arg	Pro	Gly	Met	Glu	Ile	Thr	Lys	Asp	Gly	Phe	
				140					145					150	
His	Leu	Val	Ile	Glu	Leu	Glu	Asp	Leu	Gly	Pro	Gln	Phe	Glu	Phe	
				155					160					165	
Leu	Val	Ala	Tyr	Trp	Arg	Arg	Glu	Pro	Gly	Ala	Glu	Glu	His	Val	
				170					175					180	
Lys	Met	Val	Arg	Ser	Gly	Gly	Ile	Pro	Val	His	Leu	Glu	Thr	Met	
				185					190					195	
Glu	Pro	Gly	Ala	Ala	Tyr	Cys	Val	Lys	Ala	Gln	Thr	Phe	Val	Lys	
				200					205					210	
Ala	Ile	Gly	Arg	Tyr	Ser	Ala	Phe	Ser	Gln	Thr	Glu	Cys	Val	Glu	
				215					220					225	
Val	Gln	Gly	Glu	Ala	Ile	Pro	Leu	Val	Leu	Ala	Leu	Phe	Ala	Phe	
				230					235					240	
Val	Gly	Phe	Met	Leu	Ile	Leu	Val	Val	Val	Pro	Leu	Phe	Val	Trp	
				245					250					255	
Lys	Met	Gly	Arg	Leu	Leu	Gln	Tyr	Ser	Cys	Cys	Pro	Val	Val	Val	
				260					265					270	
Leu	Pro	Asp	Thr	Leu	Lys	Ile	Thr	Asn	Ser	Pro	Gln	Lys	Leu	Ile	
				275					280					285	
Ser	Cys	Arg	Arg	Glu	Glu	Val	Asp	Ala	Cys	Ala	Thr	Ala	Val	Met	
				290					295					300	
Ser	Pro	Glu	Glu	Leu	Leu	Arg	Ala	Trp	Ile	Ser					
				305					310						

<210> 353

<211> 864

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> 654, 711, 748, 827

<223> unknown base

<400> 353

tcctgctgat gcacatctgg gtttggcaaa aggaggttgc ttcgagccgc 50

cctttctagc ttcttgcccg gctctagaac aattcaggct tcgctgcgac 100

tagacctcag ctccaacata tgcattctga agaaagatgg ctgagatgac 150

agaatgcttt attttggaaa gaaacaatgt tctaggtcaa actgagtcta 200

ccaaatgcag actttcacaa tggttctaga agaaatctgg acaagtcttt 250
 tcatgtgggtt tttctacgca ttgattccat gtttgctcac agatgaagtg 300
 gccattctgc ctgcccctca gaacctctct gtactctcaa ccaacatgaa 350
 gcatctcttg atgtggagcc cagtgatcgc gcctggagaa acagtgtact 400
 attctgtcga ataccagggg gactacgaga gcctgtacac gagccacatc 450
 tggatcccca gcagctggtg ctactcact gaaggctcctg agtgtgatgt 500
 cactgatgac atcacggcca ctgtgccata caacctttgt gtcagggcca 550
 cattgggctc acagacctca gcctggagca tcctgaagca tccctttaat 600
 agaaactcaa ccatacttac ccgacctggg atggagatca ccaaagatgg 650
 cttncacctg gttattgagc tggaggacct ggggccccag tttgagttcc 700
 ttgtggccta ntggaggagg ggcgaacccc ttgcggcgca aggggttngc 750
 gaacccttg cggccgctgg ggtatctctc gagaaaagag aggcccaata 800
 tgaccacat actcaatatg gacgaantgc tattgtccac ctgtttgagt 850
 ggcgctgggt tgat 864

- <210> 354
- <211> 23
- <212> DNA
- <213> Artificial Sequence
- <220>
- <223> Synthetic oligonucleotide probe
- <400> 354
- aggcttcgct gcgactagac ctc 23
- <210> 355
- <211> 24
- <212> DNA
- <213> Artificial Sequence
- <220>
- <223> Synthetic oligonucleotide probe
- <400> 355
- ccaggtcggg taaggatggt tgag 24
- <210> 356
- <211> 50
- <212> DNA
- <213> Artificial Sequence
- <220>
- <223> Synthetic oligonucleotide probe

<400> 356
 tttctacgca ttgattccat gtttgctcac agatgaagtg gccattctgc 50

<210> 357
 <211> 1670
 <212> DNA
 <213> Homo sapiens

<400> 357
 cccacgcgtc cgcccacgcg tccgagggac aagagagaag agagactgaa 50
 acaggagaaa gaggcaggag aggaggaggt ggggagagca cgaagctgga 100
 ggccgacact gagggagggc gggaggaggt gaagaaggag agaggggaga 150
 agaggcagga gctggaaaag agagagggag gaggaggagg agatgcggga 200
 tggagacctg gagttaggtg gcttgggaga gcttaatgaa aagagaacgg 250
 agaggaggtg tgggttagga accaagaggt agccctgtgg gcagcagaag 300
 gctgagagga gtaggaagat caggagctag agggagactg gagggttccg 350
 ggaaaagagc agaggaaaaga ggaaagacac agagagacgg gagagagaag 400
 aagagtgggt ttgaagggcg gatctcagtc cctggctgct ttggcatttg 450
 gggaaactggg actccctgtg gggaggagag gaaagctgga agtcctggag 500
 ggacagggtc ccagaaggag gggacagagg agctgagaga ggggggcagg 550
 gcgttgggca ggggtccctc ggaggcctcc tggggatggg ggctgcagct 600
 cgtctgagcg cccctcgagc gctggtactc tgggctgcac tgggggcagc 650
 agctcacatc ggaccagcac ctgaccccgga ggactggtgg agctacaagg 700
 ataatctcca gggaaacttc gtgccagggc ctcccttctg gggcctggtg 750
 aatgcagcgt ggagtctgtg tgctgtgggg aagcggcaga gccccgtgga 800
 tgtggagctg aagagggttc tttatgaccc ctttctgccc ccattaaggc 850
 tcagcactgg aggagagaag ctccggggaa ccttgtacaa caccggccga 900
 catgtctcct tcctgcctgc accccgacct gtggtcaatg tgtctggagg 950
 tccccctcct tacagccacc gactcagtga actgcggctg ctgtttggag 1000
 ctcgcgacgg agccggctcg gaacatcaga tcaaccacca gggcttctct 1050
 gctgaggtgc agctcattca cttcaaccag gaactctacg ggaatttcag 1100
 cgctgcctcc cgcgcccca atggcctggc cattctcagc ctctttgtca 1150
 acgttgccag tacctctaac ccattcctca gtcgcctcct taaccgcgac 1200
 accatcactc gcattctcta caagaatgat gcctactttc ttcaagacct 1250

gagcctggag ctctgttcc ctgaatcctt cggcttcac acctatcagg 1300
 gctctctcag caccocgccc tgctccgaga ctgtcacctg gatcctcatt 1350
 gaccggggccc tcaatatcac ctcccttcag atgcactccc tgagactcct 1400
 gagccagaat cctccatctc agatcttcca gagcctcagc ggtaacagcc 1450
 ggcccctgca gcccttggcc cacagggcac tgaggggcaa cagggacccc 1500
 cggcaccocg agaggcgctg ccgaggcccc aactaccgcc tgcatgtgga 1550
 tgggtgtcccc catggctcgt gagactcccc ttcgaggatt gcaccocgccc 1600
 gtcctaagcc tccccacaag gcgaggggag ttaccctaa aacaaagcta 1650
 ttaaaggagac agaatactta 1670

<210> 358
 <211> 328
 <212> PRT
 <213> Homo sapiens

<400> 358
 Met Gly Ala Ala Ala Arg Leu Ser Ala Pro Arg Ala Leu Val Leu
 1 5 10 15
 Trp Ala Ala Leu Gly Ala Ala Ala His Ile Gly Pro Ala Pro Asp
 20 25 30
 Pro Glu Asp Trp Trp Ser Tyr Lys Asp Asn Leu Gln Gly Asn Phe
 35 40 45
 Val Pro Gly Pro Pro Phe Trp Gly Leu Val Asn Ala Ala Trp Ser
 50 55 60
 Leu Cys Ala Val Gly Lys Arg Gln Ser Pro Val Asp Val Glu Leu
 65 70 75
 Lys Arg Val Leu Tyr Asp Pro Phe Leu Pro Pro Leu Arg Leu Ser
 80 85 90
 Thr Gly Gly Glu Lys Leu Arg Gly Thr Leu Tyr Asn Thr Gly Arg
 95 100 105
 His Val Ser Phe Leu Pro Ala Pro Arg Pro Val Val Asn Val Ser
 110 115 120
 Gly Gly Pro Leu Leu Tyr Ser His Arg Leu Ser Glu Leu Arg Leu
 125 130 135
 Leu Phe Gly Ala Arg Asp Gly Ala Gly Ser Glu His Gln Ile Asn
 140 145 150
 His Gln Gly Phe Ser Ala Glu Val Gln Leu Ile His Phe Asn Gln
 155 160 165
 Glu Leu Tyr Gly Asn Phe Ser Ala Ala Ser Arg Gly Pro Asn Gly

170	175	180
Leu Ala Ile Leu Ser Leu Phe Val Asn	Val Ala Ser Thr Ser Asn	
185	190	195
Pro Phe Leu Ser Arg Leu Leu Asn Arg	Asp Thr Ile Thr Arg Ile	
200	205	210
Ser Tyr Lys Asn Asp Ala Tyr Phe Leu	Gln Asp Leu Ser Leu Glu	
215	220	225
Leu Leu Phe Pro Glu Ser Phe Gly Phe	Ile Thr Tyr Gln Gly Ser	
230	235	240
Leu Ser Thr Pro Pro Cys Ser Glu Thr	Val Thr Trp Ile Leu Ile	
245	250	255
Asp Arg Ala Leu Asn Ile Thr Ser Leu	Gln Met His Ser Leu Arg	
260	265	270
Leu Leu Ser Gln Asn Pro Pro Ser Gln	Ile Phe Gln Ser Leu Ser	
275	280	285
Gly Asn Ser Arg Pro Leu Gln Pro Leu	Ala His Arg Ala Leu Arg	
290	295	300
Gly Asn Arg Asp Pro Arg His Pro Glu	Arg Arg Cys Arg Gly Pro	
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<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 359

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<212> DNA

<213> Artificial Sequence


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<211> 500

<212> PRT

<213> Homo sapiens

<400> 363

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				20				25						30
Leu	Leu	Glu	Lys	Leu	Leu	Glu	Lys	Tyr	Met	Asp	Glu	Asp	Gly	Glu
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Trp	Trp	Ile	Ala	Lys	Gln	Arg	Gly	Lys	Arg	Ala	Ile	Thr	Asp	Asn
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Asp	Met	Gln	Ser	Ile	Leu	Asp	Leu	His	Asn	Lys	Leu	Arg	Ser	Gln
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Val	Tyr	Pro	Thr	Ala	Ser	Asn	Met	Glu	Tyr	Met	Thr	Trp	Asp	Val
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Glu	Leu	Glu	Arg	Ser	Ala	Glu	Ser	Trp	Ala	Glu	Ser	Cys	Leu	Trp
				95				100						105
Glu	His	Gly	Pro	Ala	Ser	Leu	Leu	Pro	Ser	Ile	Gly	Gln	Asn	Leu
				110				115						120
Gly	Ala	His	Trp	Gly	Arg	Tyr	Arg	Pro	Pro	Thr	Phe	His	Val	Gln
				125				130						135
Ser	Trp	Tyr	Asp	Glu	Val	Lys	Asp	Phe	Ser	Tyr	Pro	Tyr	Glu	His
				140				145						150
Glu	Cys	Asn	Pro	Tyr	Cys	Pro	Phe	Arg	Cys	Ser	Gly	Pro	Val	Cys
				155				160						165
Thr	His	Tyr	Thr	Gln	Val	Val	Trp	Ala	Thr	Ser	Asn	Arg	Ile	Gly

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Cys	Ala	Ile	Asn	Leu	Cys	His	Asn	Met	Asn	Ile	Trp	Gly	Gln	Ile
				185					190					195
Trp	Pro	Lys	Ala	Val	Tyr	Leu	Val	Cys	Asn	Tyr	Ser	Pro	Lys	Gly
				200					205					210
Asn	Trp	Trp	Gly	His	Ala	Pro	Tyr	Lys	His	Gly	Arg	Pro	Cys	Ser
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Ala	Cys	Pro	Pro	Ser	Phe	Gly	Gly	Gly	Cys	Arg	Glu	Asn	Leu	Cys
				230					235					240
Tyr	Lys	Glu	Gly	Ser	Asp	Arg	Tyr	Tyr	Pro	Pro	Arg	Glu	Glu	Glu
				245					250					255
Thr	Asn	Glu	Ile	Glu	Arg	Gln	Gln	Ser	Gln	Val	His	Asp	Thr	His
				260					265					270
Val	Arg	Thr	Arg	Ser	Asp	Asp	Ser	Ser	Arg	Asn	Glu	Val	Ile	Ser
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Ala	Gln	Gln	Met	Ser	Gln	Ile	Val	Ser	Cys	Glu	Val	Arg	Leu	Arg
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Asp	Gln	Cys	Lys	Gly	Thr	Thr	Cys	Asn	Arg	Tyr	Glu	Cys	Pro	Ala
				305					310					315
Gly	Cys	Leu	Asp	Ser	Lys	Ala	Lys	Val	Ile	Gly	Ser	Val	His	Tyr
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Glu	Met	Gln	Ser	Ser	Ile	Cys	Arg	Ala	Ala	Ile	His	Tyr	Gly	Ile
				335					340					345
Ile	Asp	Asn	Asp	Gly	Gly	Trp	Val	Asp	Ile	Thr	Arg	Gln	Gly	Arg
				350					355					360
Lys	His	Tyr	Phe	Ile	Lys	Ser	Asn	Arg	Asn	Gly	Ile	Gln	Thr	Ile
				365					370					375
Gly	Lys	Tyr	Gln	Ser	Ala	Asn	Ser	Phe	Thr	Val	Ser	Lys	Val	Thr
				380					385					390
Val	Gln	Ala	Val	Thr	Cys	Glu	Thr	Thr	Val	Glu	Gln	Leu	Cys	Pro
				395					400					405
Phe	His	Lys	Pro	Ala	Ser	His	Cys	Pro	Arg	Val	Tyr	Cys	Pro	Arg
				410					415					420
Asn	Cys	Met	Gln	Ala	Asn	Pro	His	Tyr	Ala	Arg	Val	Ile	Gly	Thr
				425					430					435
Arg	Val	Tyr	Ser	Asp	Leu	Ser	Ser	Ile	Cys	Arg	Ala	Ala	Val	His
				440					445					450
Ala	Gly	Val	Val	Arg	Asn	His	Gly	Gly	Tyr	Val	Asp	Val	Met	Pro
				455					460					465

240

Val	Asp	Lys	Arg	Lys	Thr	Tyr	Ile	Ala	Ser	Phe	Gln	Asn	Gly	Ile
				470					475				480	
Phe	Ser	Glu	Ser	Leu	Gln	Asn	Pro	Pro	Gly	Gly	Lys	Ala	Phe	Arg
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<220>
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<400> 365
 ccaagagtat actgtcctcg 20

<210> 366
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 <212> DNA
 <213> Artificial Sequence

<220>
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<400> 366
 agcacagatt ttctctacag ccccc 25

<210> 367
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<400> 367
 aaccactcca gcatgtactg ctgc 24

<210> 368
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<212> DNA
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 <212> PRT
 <213> Homo sapiens

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 35 40 45
 Ile Arg Tyr Ser Asp Val Lys Lys Leu Glu Met Lys Pro Lys Tyr
 50 55 60
 Pro His Cys Glu Glu Lys Met Val Ile Ile Thr Thr Lys Ser Val
 65 70 75
 Ser Arg Tyr Arg Gly Gln Glu His Cys Leu His Pro Lys Leu Gln
 80 85 90
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 Arg Arg Val Tyr Glu Glu
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<400> 371

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<210> 372

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<212> DNA

<213> Artificial Sequence

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<223> Synthetic oligonucleotide probe

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<212> DNA

<213> Homo sapiens

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<211> 816

<212> PRT

<213> Homo sapiens

<400> 375

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Lys	Phe	Thr	Leu	Ile	Asp	Ser	Gln	Ala	Gln	Tyr	Pro	Val	Val	Asn
			20						25					30

Thr	Asn	Tyr	Gly	Lys	Ile	Arg	Gly	Leu	Arg	Thr	Pro	Leu	Pro	Asn
			35					40						45

Glu	Ile	Leu	Gly	Pro	Val	Glu	Gln	Tyr	Leu	Gly	Val	Pro	Tyr	Ala
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

				50					55					60	
Ser	Pro	Pro	Thr	Gly	Glu	Arg	Arg	Phe	Gln	Pro	Pro	Glu	Pro	Pro	
				65					70					75	
Ser	Ser	Trp	Thr	Gly	Ile	Arg	Asn	Thr	Thr	Gln	Phe	Ala	Ala	Val	
				80					85					90	
Cys	Pro	Gln	His	Leu	Asp	Glu	Arg	Ser	Leu	Leu	His	Asp	Met	Leu	
				95					100					105	
Pro	Ile	Trp	Phe	Thr	Ala	Asn	Leu	Asp	Thr	Leu	Met	Thr	Tyr	Val	
				110					115					120	
Gln	Asp	Gln	Asn	Glu	Asp	Cys	Leu	Tyr	Leu	Asn	Ile	Tyr	Val	Pro	
				125					130					135	
Thr	Glu	Asp	Gly	Ala	Asn	Thr	Lys	Lys	Asn	Ala	Asp	Asp	Ile	Thr	
				140					145					150	
Ser	Asn	Asp	Arg	Gly	Glu	Asp	Glu	Asp	Ile	His	Asp	Gln	Asn	Ser	
				155					160					165	
Lys	Lys	Pro	Val	Met	Val	Tyr	Ile	His	Gly	Gly	Ser	Tyr	Met	Glu	
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Gly	Thr	Gly	Asn	Met	Ile	Asp	Gly	Ser	Ile	Leu	Ala	Ser	Tyr	Gly	
				185					190					195	
Asn	Val	Ile	Val	Ile	Thr	Ile	Asn	Tyr	Arg	Leu	Gly	Ile	Leu	Gly	
				200					205					210	
Phe	Leu	Ser	Thr	Gly	Asp	Gln	Ala	Ala	Lys	Gly	Asn	Tyr	Gly	Leu	
				215					220					225	
Leu	Asp	Gln	Ile	Gln	Ala	Leu	Arg	Trp	Ile	Glu	Glu	Asn	Val	Gly	
				230					235					240	
Ala	Phe	Gly	Gly	Asp	Pro	Lys	Arg	Val	Thr	Ile	Phe	Gly	Ser	Gly	
				245					250					255	
Ala	Gly	Ala	Ser	Cys	Val	Ser	Leu	Leu	Thr	Leu	Ser	His	Tyr	Ser	
				260					265					270	
Glu	Gly	Leu	Phe	Gln	Lys	Ala	Ile	Ile	Gln	Ser	Gly	Thr	Ala	Leu	
				275					280					285	
Ser	Ser	Trp	Ala	Val	Asn	Tyr	Gln	Pro	Ala	Lys	Tyr	Thr	Arg	Ile	
				290					295					300	
Leu	Ala	Asp	Lys	Val	Gly	Cys	Asn	Met	Leu	Asp	Thr	Thr	Asp	Met	
				305					310					315	
Val	Glu	Cys	Leu	Arg	Asn	Lys	Asn	Tyr	Lys	Glu	Leu	Ile	Gln	Gln	
				320					325					330	
Thr	Ile	Thr	Pro	Ala	Thr	Tyr	His	Ile	Ala	Phe	Gly	Pro	Val	Ile	
				335					340					345	

Asp Gly Asp Val	Ile Pro Asp Asp Pro	Gln Ile Leu Met Glu Gln	350	355	360
Gly Glu Phe Leu	Asn Tyr Asp Ile Met	Leu Gly Val Asn Gln Gly	365	370	375
Glu Gly Leu Lys	Phe Val Asp Gly Ile	Val Asp Asn Glu Asp Gly	380	385	390
Val Thr Pro Asn	Asp Phe Asp Phe Ser	Val Ser Asn Phe Val Asp	395	400	405
Asn Leu Tyr Gly	Tyr Pro Glu Gly Lys	Asp Thr Leu Arg Glu Thr	410	415	420
Ile Lys Phe Met	Tyr Thr Asp Trp Ala	Asp Lys Glu Asn Pro Glu	425	430	435
Thr Arg Arg Lys	Thr Leu Val Ala Leu	Phe Thr Asp His Gln Trp	440	445	450
Val Ala Pro Ala	Val Ala Ala Asp Leu	His Ala Gln Tyr Gly Ser	455	460	465
Pro Thr Tyr Phe	Tyr Ala Phe Tyr His	His Cys Gln Ser Glu Met	470	475	480
Lys Pro Ser Trp	Ala Asp Ser Ala His	Gly Asp Glu Val Pro Tyr	485	490	495
Val Phe Gly Ile	Pro Met Ile Gly Pro	Thr Glu Leu Phe Ser Cys	500	505	510
Asn Phe Ser Lys	Asn Asp Val Met Leu	Ser Ala Val Val Met Thr	515	520	525
Tyr Trp Thr Asn	Phe Ala Lys Thr Gly	Asp Pro Asn Gln Pro Val	530	535	540
Pro Gln Asp Thr	Lys Phe Ile His Thr	Lys Pro Asn Arg Phe Glu	545	550	555
Glu Val Ala Trp	Ser Lys Tyr Asn Pro	Lys Asp Gln Leu Tyr Leu	560	565	570
His Ile Gly Leu	Lys Pro Arg Val Arg	Asp His Tyr Arg Ala Thr	575	580	585
Lys Val Ala Phe	Trp Leu Glu Leu Val	Pro His Leu His Asn Leu	590	595	600
Asn Glu Ile Phe	Gln Tyr Val Ser Thr	Thr Thr Lys Val Pro Pro	605	610	615
Pro Asp Met Thr	Ser Phe Pro Tyr Gly	Thr Arg Arg Ser Pro Ala	620	625	630
Lys Ile Trp Pro	Thr Thr Lys Arg Pro	Ala Ile Thr Pro Ala Asn			

635	640	645
Asn Pro Lys His Ser Lys Asp Pro His Lys Thr Gly Pro Glu Asp		
650	655	660
Thr Thr Val Leu Ile Glu Thr Lys Arg Asp Tyr Ser Thr Glu Leu		
665	670	675
Ser Val Thr Ile Ala Val Gly Ala Ser Leu Leu Phe Leu Asn Ile		
680	685	690
Leu Ala Phe Ala Ala Leu Tyr Tyr Lys Lys Asp Lys Arg Arg His		
695	700	705
Glu Thr His Arg Arg Pro Ser Pro Gln Arg Asn Thr Thr Asn Asp		
710	715	720
Ile Ala His Ile Gln Asn Glu Glu Ile Met Ser Leu Gln Met Lys		
725	730	735
Gln Leu Glu His Asp His Glu Cys Glu Ser Leu Gln Ala His Asp		
740	745	750
Thr Leu Arg Leu Thr Cys Pro Pro Asp Tyr Thr Leu Thr Leu Arg		
755	760	765
Arg Ser Pro Asp Asp Ile Pro Leu Met Thr Pro Asn Thr Ile Thr		
770	775	780
Met Ile Pro Asn Thr Leu Thr Gly Met Gln Pro Leu His Thr Phe		
785	790	795
Asn Thr Phe Ser Gly Gly Gln Asn Ser Thr Asn Leu Pro His Gly		
800	805	810
His Ser Thr Thr Arg Val		
815		

<210> 376
 <211> 25
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 376
 ggcaagctac ggaaacgtca tcgtg 25

<210> 377
 <211> 25
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 377

aacccccgag ccaaaagatg gtcac 25

<210> 378

<211> 47

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 378

gtaccggtga ccaggcagca aaaggcaact atgggctcct ggatcag 47

<210> 379

<211> 2461

<212> DNA

<213> Homo sapiens

<400> 379

gggaaagatg gcggcgactc tgggaccct tgggtcgtgg cagcagtggc 50

ggcgatgttt gtcggctcgg gatgggtcca ggatgttact ccttcttctt 100

ttgttggggt ctgggcaggg gccacagcaa gtcggggcgg gtcaaacgtt 150

cgagtacttg aaacgggagc actcgctgtc gaagccctac cagggtgtgg 200

gcacaggcag ttcctcactg tggaaatctga tgggcaatgc catggtgatg 250

accaggtata tccgccttac ccagatatg caaagtaaac aggggtgcctt 300

gtggaaccgg gtgccatgtt tcttgagaga ctgggagttg cagggtgcact 350

tcaaaatcca tggacaagga aagaagaatc tgcattgggga tggcttggca 400

atctggtaca caaaggatcg gatgcagcca gggcctgtgt ttggaacat 450

ggacaaattt gtggggctgg gagtatttgt agacacctac cccaatgagg 500

agaagcagca agagcgggta tccccctaca tctcagccat ggtgaacaac 550

ggctccctca gctatgatca tgagcgggat gggcggccta cagagctggg 600

aggctgcaca gccattgtcc gcaatcttca ttacgacacc ttcctggtga 650

ttcgctacgt caagaggcat ttgacgataa tgatggatat tgatggcaag 700

catgagtgga gggactgcat tgaagtgccg ggagtccgcc tgccccgcgg 750

ctactacttc ggcaacctct ccactactgg ggatctctca gataatcatg 800

atgtcatttc cttgaagttg tttgaactga cagtggagag aacccagaa 850

gaggaaaagc tccatcgaga tgtgttcttg ccctcagtgg acaatatgaa 900

gctgcctgag atgacagctc cactgccgcc cctgagtggc ctggccctct 950

tctcatcgtg ctttttctcc ctggtgtttt ctgtatttgc catagtcatt 1000

ggtatcatac tctacaacaa atggcaggaa cagagccgaa agcgcttcta 1050
 ctgagccctc ctgctgccac cacttttgtg actgtcacc c atgaggtatg 1100
 gaaggagcag gcactggcct gagcatgcag cctggagagt gttcttgtct 1150
 ctagcagctg gttggggact atattctgtc actggagttt tgaatgcagg 1200
 gaccccgcat tcccatgggt gtgcatgggg acatctaact ctggtctggg 1250
 aagccacca cccagggca atgctgctgt gatgtgcctt tccctgcagt 1300
 ccttccatgt gggagcagag gtgtgaagag aatttacgtg gttgtgatgc 1350
 caaaatcaca gaacagaatt tcatagccca ggctgccgtg ttgtttgact 1400
 cagaaggccc ttctacttca gttttgaatc cacaaagaat taaaaactgg 1450
 taacaccaca ggcttttctga ccatccattc gttgggtttt gcatttgacc 1500
 caaccctctg cctacctgag gagctttctt tggaaaccag gatggaaact 1550
 tcttccctgc cttaccttc tttcactcca ttcattgtcc tctctgtgtg 1600
 caacctgagc tgggaaaggc atttggatgc ctctctgttg gggcctgggg 1650
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 ttggcatgtc catggccttc ccaatcaagt ctcttcaggc cctcagtga 1800
 gtttggtctaa aggttgggtg aaaaatcaag agaagcctgg aagacatcat 1850
 ggatgccatg gattagctgt gcaactgacc agctccaggt ttgatcaaac 1900
 caaaagcaac atttgtcatg tgggtctgacc atgtggagat gtttctggac 1950
 ttgctagagc ctgcttagct gcatgttttg tagttacgat ttttggaatc 2000
 ccactttgag tgctgaaagt gtaaggaagc tttcttctta caccttgggc 2050
 ttggatattg ccagagaag aaatttggct tttttttct taatggacaa 2100
 gagacagttg ctgttctcat gttccaagtc tgagagcaac agaccctcat 2150
 catctgtgcc tggaagagtt cactgtcatt gagcagcaca gcctgagtgc 2200
 tggcctctgt caacccttat tccactgcct tatttgacaa ggggttacat 2250
 gctgctcacc ttactgcctt gggattaaat cagttacagg ccagagtctc 2300
 cttggagggc ctggaactct gagtctcct atgaacctct gtagcctaaa 2350
 tgaaattctt aaaatcaccg atggaaccaa aaaaaaaaaa aaaaaggcg 2400
 gccgcgactc tagagtogac ctgcagtagg gataacagg taataagctt 2450

ggccgccatg g 2461

<210> 380

<211> 348

<212> PRT

<213> Homo sapiens

<400> 380

Met	Ala	Ala	Thr	Leu	Gly	Pro	Leu	Gly	Ser	Trp	Gln	Gln	Trp	Arg	
1				5					10					15	
Arg	Cys	Leu	Ser	Ala	Arg	Asp	Gly	Ser	Arg	Met	Leu	Leu	Leu	Leu	
				20					25					30	
Leu	Leu	Leu	Gly	Ser	Gly	Gln	Gly	Pro	Gln	Gln	Val	Gly	Ala	Gly	
				35					40					45	
Gln	Thr	Phe	Glu	Tyr	Leu	Lys	Arg	Glu	His	Ser	Leu	Ser	Lys	Pro	
				50					55					60	
Tyr	Gln	Gly	Val	Gly	Thr	Gly	Ser	Ser	Ser	Leu	Trp	Asn	Leu	Met	
				65					70					75	
Gly	Asn	Ala	Met	Val	Met	Thr	Gln	Tyr	Ile	Arg	Leu	Thr	Pro	Asp	
				80					85					90	
Met	Gln	Ser	Lys	Gln	Gly	Ala	Leu	Trp	Asn	Arg	Val	Pro	Cys	Phe	
				95					100					105	
Leu	Arg	Asp	Trp	Glu	Leu	Gln	Val	His	Phe	Lys	Ile	His	Gly	Gln	
				110					115					120	
Gly	Lys	Lys	Asn	Leu	His	Gly	Asp	Gly	Leu	Ala	Ile	Trp	Tyr	Thr	
				125					130					135	
Lys	Asp	Arg	Met	Gln	Pro	Gly	Pro	Val	Phe	Gly	Asn	Met	Asp	Lys	
				140					145					150	
Phe	Val	Gly	Leu	Gly	Val	Phe	Val	Asp	Thr	Tyr	Pro	Asn	Glu	Glu	
				155					160					165	
Lys	Gln	Gln	Glu	Arg	Val	Phe	Pro	Tyr	Ile	Ser	Ala	Met	Val	Asn	
				170					175					180	
Asn	Gly	Ser	Leu	Ser	Tyr	Asp	His	Glu	Arg	Asp	Gly	Arg	Pro	Thr	
				185					190					195	
Glu	Leu	Gly	Gly	Cys	Thr	Ala	Ile	Val	Arg	Asn	Leu	His	Tyr	Asp	
				200					205					210	
Thr	Phe	Leu	Val	Ile	Arg	Tyr	Val	Lys	Arg	His	Leu	Thr	Ile	Met	
				215					220					225	
Met	Asp	Ile	Asp	Gly	Lys	His	Glu	Trp	Arg	Asp	Cys	Ile	Glu	Val	
				230					235					240	
Pro	Gly	Val	Arg	Leu	Pro	Arg	Gly	Tyr	Tyr	Phe	Gly	Thr	Ser	Ser	
				245					250					255	

Ile Thr Gly Asp Leu Ser Asp Asn His Asp Val Ile Ser Leu Lys	260	265	270
Leu Phe Glu Leu Thr Val Glu Arg Thr Pro Glu Glu Glu Lys Leu	275	280	285
His Arg Asp Val Phe Leu Pro Ser Val Asp Asn Met Lys Leu Pro	290	295	300
Glu Met Thr Ala Pro Leu Pro Pro Leu Ser Gly Leu Ala Leu Phe	305	310	315
Leu Ile Val Phe Phe Ser Leu Val Phe Ser Val Phe Ala Ile Val	320	325	330
Ile Gly Ile Ile Leu Tyr Asn Lys Trp Gln Glu Gln Ser Arg Lys	335	340	345

Arg Phe Tyr

<210> 381
 <211> 22
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 381
 ccttgggtcg tggcagcagt gg 22

<210> 382
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 382
 cactctccag gctgcatgct cagg 24

<210> 383
 <211> 45
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 383
 gtcaaacggtt cgagtacttg aaacgggagc actcgctgtc gaagc 45

<210> 384
 <211> 3150
 <212> DNA
 <213> Homo sapiens

<400> 384

ccgagccggg cgcgcagcga cggagctggg gccggcctgg gaccatgggc 50
 gtgagtgcaa tctacggatc agtctctgat ggtgggtcgt taacctcagt 100
 ggggactcca agatttccat gaagaaaatc agttgtcttc attcaagaat 150
 tggggctctgg ctcaagaattc ctgcagctgg tgaaaatctg ttttctagaa 200
 gaggtttaat taatgcctgc agtctgacat gttcccgatt tgaggtgaaa 250
 ccatgaagag aaaatagaat acttaataat gcttttccgc aaccgcttct 300
 tgctgtctgt ggccctggct gcgctgctgg cctttgtgag cctcagcctg 350
 cagttcttcc acctgatccc ggtgtcgact cctaagaatg gaatgagtag 400
 caagagtcga aagagaatca tgccccgacc tgtgacggag cccoctgtga 450
 cagaccccggt ttatgaagct cttttgtact gcaacatccc cagtgtggcc 500
 gagcgcagca tggaaggcca tgccccgcat cattttaagc tggctctcagt 550
 gcatgtgttc attcgccacg gagacaggta cccactgtat gtcattccca 600
 aaacaaagcg accagaaatt gactgcactc tgggtggctaa caggaaaccg 650
 tatcacccaa aactggaagc tttcattagt cacatgtcaa aaggatccgg 700
 agcctctttc gaaagcccct tgaactcctt gcctctttac ccaaatacc 750
 cattgtgtga gatgggagag ctcacacaga caggagtgtg gcagcatttg 800
 cagaacggtc agctgctgag ggatatctat ctaaagaaac acaaactcct 850
 gccaatgat tggctctgcag accagctcta tttagagacc actgggaaaa 900
 gccggaccct acaaagtggg ctggccttgc tttatggctt tctcccagat 950
 tttgactgga agaagattta tttcaggcac cagccaagtg cgctgttctg 1000
 ctctggaagc tgctattgcc cggttaagaa ccagtatctg gaaaaggagc 1050
 agcgtcgtca gtacctcta cgtttgaaaa acagccagct ggagaagacc 1100
 tacggggaga tggccaagat cgtggatgtc cccaccaagc agcttagagc 1150
 tgccaacccc atagactcca tgctctgcc cttctgccac aatgtcagct 1200
 ttccctgtac cagaaatggc tgtgttgaca tggagcactt caaggtatt 1250
 aagaccatc agatcgagga tgaaagggaa agacgggaga agaaattgta 1300
 cttcgggtat tctctctgg gtgcccacc catcctgaac caaaccatcg 1350
 gccgatgca gcgtgccacc gagggcagga aagaagagct ctttgccctc 1400
 tactctgctc atgatgtcac tctgtcacca gttctcagtg ccttgggcct 1450

attgattttt aaatgcgttt ttggaagaac ttgctatta ggtagtttac 2950
 agatctttat aaggtgtttt atatattaga agcaattata attacatctg 3000
 tgattttctga actaatggtg ctaattcaga gaaatggaaa gtgaaagtga 3050
 gattctctgt tgtcatcggc attccaactt tttctctttg tttttgtcca 3100
 gtgttgcatc tgaatatgtc tgtttctata aataaatttt ttaagaataa 3150

<210> 385

<211> 480

<212> PRT

<213> Homo sapiens

<400> 385

Met	Leu	Phe	Arg	Asn	Arg	Phe	Leu	Leu	Leu	Leu	Ala	Leu	Ala	Ala	1	5	10	15
Leu	Leu	Ala	Phe	Val	Ser	Leu	Ser	Leu	Gln	Phe	Phe	His	Leu	Ile	20	25	30	
Pro	Val	Ser	Thr	Pro	Lys	Asn	Gly	Met	Ser	Ser	Lys	Ser	Arg	Lys	35	40	45	
Arg	Ile	Met	Pro	Asp	Pro	Val	Thr	Glu	Pro	Pro	Val	Thr	Asp	Pro	50	55	60	
Val	Tyr	Glu	Ala	Leu	Leu	Tyr	Cys	Asn	Ile	Pro	Ser	Val	Ala	Glu	65	70	75	
Arg	Ser	Met	Glu	Gly	His	Ala	Pro	His	His	Phe	Lys	Leu	Val	Ser	80	85	90	
Val	His	Val	Phe	Ile	Arg	His	Gly	Asp	Arg	Tyr	Pro	Leu	Tyr	Val	95	100	105	
Ile	Pro	Lys	Thr	Lys	Arg	Pro	Glu	Ile	Asp	Cys	Thr	Leu	Val	Ala	110	115	120	
Asn	Arg	Lys	Pro	Tyr	His	Pro	Lys	Leu	Glu	Ala	Phe	Ile	Ser	His	125	130	135	
Met	Ser	Lys	Gly	Ser	Gly	Ala	Ser	Phe	Glu	Ser	Pro	Leu	Asn	Ser	140	145	150	
Leu	Pro	Leu	Tyr	Pro	Asn	His	Pro	Leu	Cys	Glu	Met	Gly	Glu	Leu	155	160	165	
Thr	Gln	Thr	Gly	Val	Val	Gln	His	Leu	Gln	Asn	Gly	Gln	Leu	Leu	170	175	180	
Arg	Asp	Ile	Tyr	Leu	Lys	Lys	His	Lys	Leu	Leu	Pro	Asn	Asp	Trp	185	190	195	
Ser	Ala	Asp	Gln	Leu	Tyr	Leu	Glu	Thr	Thr	Gly	Lys	Ser	Arg	Thr	200	205	210	

Leu	Gln	Ser	Gly	Leu	Ala	Leu	Leu	Tyr	Gly	Phe	Leu	Pro	Asp	Phe	
				215					220					225	
Asp	Trp	Lys	Lys	Ile	Tyr	Phe	Arg	His	Gln	Pro	Ser	Ala	Leu	Phe	
				230					235					240	
Cys	Ser	Gly	Ser	Cys	Tyr	Cys	Pro	Val	Arg	Asn	Gln	Tyr	Leu	Glu	
				245					250					255	
Lys	Glu	Gln	Arg	Arg	Gln	Tyr	Leu	Leu	Arg	Leu	Lys	Asn	Ser	Gln	
				260					265					270	
Leu	Glu	Lys	Thr	Tyr	Gly	Glu	Met	Ala	Lys	Ile	Val	Asp	Val	Pro	
				275					280					285	
Thr	Lys	Gln	Leu	Arg	Ala	Ala	Asn	Pro	Ile	Asp	Ser	Met	Leu	Cys	
				290					295					300	
His	Phe	Cys	His	Asn	Val	Ser	Phe	Pro	Cys	Thr	Arg	Asn	Gly	Cys	
				305					310					315	
Val	Asp	Met	Glu	His	Phe	Lys	Val	Ile	Lys	Thr	His	Gln	Ile	Glu	
				320					325					330	
Asp	Glu	Arg	Glu	Arg	Arg	Glu	Lys	Lys	Leu	Tyr	Phe	Gly	Tyr	Ser	
				335					340					345	
Leu	Leu	Gly	Ala	His	Pro	Ile	Leu	Asn	Gln	Thr	Ile	Gly	Arg	Met	
				350					355					360	
Gln	Arg	Ala	Thr	Glu	Gly	Arg	Lys	Glu	Glu	Leu	Phe	Ala	Leu	Tyr	
				365					370					375	
Ser	Ala	His	Asp	Val	Thr	Leu	Ser	Pro	Val	Leu	Ser	Ala	Leu	Gly	
				380					385					390	
Leu	Ser	Glu	Ala	Arg	Phe	Pro	Arg	Phe	Ala	Ala	Arg	Leu	Ile	Phe	
				395					400					405	
Glu	Leu	Trp	Gln	Asp	Arg	Glu	Lys	Pro	Ser	Glu	His	Ser	Val	Arg	
				410					415					420	
Ile	Leu	Tyr	Asn	Gly	Val	Asp	Val	Thr	Phe	His	Thr	Ser	Phe	Cys	
				425					430					435	
Gln	Asp	His	His	Lys	Arg	Ser	Pro	Lys	Pro	Met	Cys	Pro	Leu	Glu	
				440					445					450	
Asn	Leu	Val	Arg	Phe	Val	Lys	Arg	Asp	Met	Phe	Val	Ala	Leu	Gly	
				455					460					465	
Gly	Ser	Gly	Thr	Asn	Tyr	Tyr	Asp	Ala	Cys	His	Arg	Glu	Gly	Phe	
				470					475					480	

<210> 386

<211> 24

<212> DNA

<213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe
 <400> 386
 ccaagcagct tagagctcca gacc 24
 <210> 387
 <211> 25
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe
 <400> 387
 ttccctatgc tctgtattgg catgg 25
 <210> 388
 <211> 50
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe
 <400> 388
 gccacttctg ccacaatgtc agctttccct gtaccagaaa tggctgtgtt 50
 <210> 389
 <211> 3313
 <212> DNA
 <213> Homo sapiens

<400> 389
 aaaaaagctc actaaagttt ctattagagc gaatacggta gatttccatc 50
 cccttttgaa gaacagtact gtggagctat ttaagagata aaaacgaaat 100
 atcctttctg ggagttcaag attgtgcagt aattggttag gactctgagc 150
 gccgctgttc accaatcggg gagagaaaag cggagatcct gctcgccctg 200
 cacgcgcctg aagcacaaag cagatagcta ggaatgaacc atccctggga 250
 gtatgtggaa acaacggagg agctctgact tcccaactgt cccattctat 300
 gggcgaagga actgctcctg acttcagtgg ttaagggcag aattgaaaat 350
 aattctggag gaagataaga atgattcctg cgcgactgca ccgggactac 400
 aaagggcttg tctgctggg aatcctcctg gggactctgt gggagaccgg 450
 atgcaccag atacgtatt cagttccgga agagctggag aaaggctcta 500
 ggggtgggcga catctccagg gacctggggc tggagccccg ggagctcgcg 550
 gagcgcggag tccgcatcat cccagaggt aggacgcagc ttttcgccct 600

gaatccgcgc agcggcagct tggtcacggc gggcaggata gaccgggagg 650
 agctctgtat gggggccatc aagtgtcaat taaatctaga cattctgatg 700
 gaggataaaag tgaaaatata tggagtagaa gtagaagtaa gggacattaa 750
 cgacaatgcg ccttactttc gtgaaagtga attagaaata aaaattagtg 800
 aaaatgcagc cactgagatg cggttccctc taccacacgc ctgggatccg 850
 gatatcggga agaactctct gcagagctac gagctcagcc cgaacactca 900
 cttctccctc atcgtgcaaa atggagccga cggtagtaag taccocgaat 950
 tgggtgctgaa acgcgccttg gaccgcgaag aaaaggctgc tcaccacctg 1000
 gtccttacgg cctccgacgg gggcgacccg gtgcgcacag gcaccgcgcg 1050
 catccgcgtg atggttcttg atgcgaacga caacgcacca gcgtttgctc 1100
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 ctgctttagt tcaacgctac cgaccctgac gaaggagtca atgcggaagt 1200
 gaggtattcc ttcoggtatg tggacgacaa ggcggcccaa gttttcaaac 1250
 tagattgtaa ttcagggaca atatcaacaa taggggagtt ggaccacgag 1300
 gagtcaggat tctaccagat ggaagtgcaa gcaatggata atgcaggata 1350
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<210> 390
 <211> 916
 <212> PRT
 <213> Homo sapiens
 <400> 390

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Leu	Gly	Ile	Leu	Leu	Gly	Thr	Leu	Trp	Glu	Thr	Gly	Cys	Thr	Gln	
				20					25					30	
Ile	Arg	Tyr	Ser	Val	Pro	Glu	Glu	Leu	Glu	Lys	Gly	Ser	Arg	Val	
				35					40					45	
Gly	Asp	Ile	Ser	Arg	Asp	Leu	Gly	Leu	Glu	Pro	Arg	Glu	Leu	Ala	
				50					55					60	
Glu	Arg	Gly	Val	Arg	Ile	Ile	Pro	Arg	Gly	Arg	Thr	Gln	Leu	Phe	
				65					70					75	
Ala	Leu	Asn	Pro	Arg	Ser	Gly	Ser	Leu	Val	Thr	Ala	Gly	Arg	Ile	
				80					85					90	
Asp	Arg	Glu	Glu	Leu	Cys	Met	Gly	Ala	Ile	Lys	Cys	Gln	Leu	Asn	
				95					100					105	
Leu	Asp	Ile	Leu	Met	Glu	Asp	Lys	Val	Lys	Ile	Tyr	Gly	Val	Glu	
				110					115					120	
Val	Glu	Val	Arg	Asp	Ile	Asn	Asp	Asn	Ala	Pro	Tyr	Phe	Arg	Glu	
				125					130					135	
Ser	Glu	Leu	Glu	Ile	Lys	Ile	Ser	Glu	Asn	Ala	Ala	Thr	Glu	Met	
				140					145					150	
Arg	Phe	Pro	Leu	Pro	His	Ala	Trp	Asp	Pro	Asp	Ile	Gly	Lys	Asn	
				155					160					165	
Ser	Leu	Gln	Ser	Tyr	Glu	Leu	Ser	Pro	Asn	Thr	His	Phe	Ser	Leu	
				170					175					180	
Ile	Val	Gln	Asn	Gly	Ala	Asp	Gly	Ser	Lys	Tyr	Pro	Glu	Leu	Val	
				185					190					195	
Leu	Lys	Arg	Ala	Leu	Asp	Arg	Glu	Glu	Lys	Ala	Ala	His	His	Leu	
				200					205					210	
Val	Leu	Thr	Ala	Ser	Asp	Gly	Gly	Asp	Pro	Val	Arg	Thr	Gly	Thr	
				215					220					225	
Ala	Arg	Ile	Arg	Val	Met	Val	Leu	Asp	Ala	Asn	Asp	Asn	Ala	Pro	
				230					235					240	
Ala	Phe	Ala	Gln	Pro	Glu	Tyr	Arg	Ala	Ser	Val	Pro	Glu	Asn	Leu	
				245					250					255	
Ala	Leu	Gly	Thr	Gln	Leu	Leu	Val	Val	Asn	Ala	Thr	Asp	Pro	Asp	
				260					265					270	
Glu	Gly	Val	Asn	Ala	Glu	Val	Arg	Tyr	Ser	Phe	Arg	Tyr	Val	Asp	
				275					280					285	
Asp	Lys	Ala	Ala	Gln	Val	Phe	Lys	Leu	Asp	Cys	Asn	Ser	Gly	Thr	

	290		295		300
Ile Ser Thr Ile	Gly Glu Leu Asp His	Glu Glu Ser Gly Phe Tyr			
	305	310			315
Gln Met Glu Val	Gln Ala Met Asp Asn	Ala Gly Tyr Ser Ala Arg			
	320	325			330
Ala Lys Val Leu	Ile Thr Val Leu Asp	Val Asn Asp Asn Ala Pro			
	335	340			345
Glu Val Val Leu	Thr Ser Leu Ala Ser	Ser Val Pro Glu Asn Ser			
	350	355			360
Pro Arg Gly Thr	Leu Ile Ala Leu Leu	Asn Val Asn Asp Gln Asp			
	365	370			375
Ser Glu Glu Asn	Gly Gln Val Ile Cys	Phe Ile Gln Gly Asn Leu			
	380	385			390
Pro Phe Lys Leu	Gly Lys Ser Tyr Gly	Asn Tyr Tyr Ser Leu Val			
	395	400			405
Thr Asp Ile Val	Leu Asp Arg Glu Gln	Val Pro Ser Tyr Asn Ile			
	410	415			420
Thr Val Thr Ala	Thr Asp Arg Gly Thr	Pro Pro Leu Ser Thr Glu			
	425	430			435
Thr His Ile Ser	Leu Asn Val Ala Asp	Thr Asn Asp Asn Pro Pro			
	440	445			450
Val Phe Pro Gln	Ala Ser Tyr Ser Ala	Tyr Ile Pro Glu Asn Asn			
	455	460			465
Pro Arg Gly Val	Ser Leu Val Ser Val	Thr Ala His Asp Pro Asp			
	470	475			480
Cys Glu Glu Asn	Ala Gln Ile Thr Tyr	Ser Leu Ala Glu Asn Thr			
	485	490			495
Ile Gln Gly Ala	Ser Leu Ser Ser Tyr	Val Ser Ile Asn Ser Asp			
	500	505			510
Thr Gly Val Leu	Tyr Ala Leu Ser Ser	Phe Asp Tyr Glu Gln Phe			
	515	520			525
Arg Asp Leu Gln	Val Lys Val Met Ala	Arg Asp Asn Gly His Pro			
	530	535			540
Pro Leu Ser Ser	Asn Val Ser Leu Ser	Leu Phe Val Leu Asp Gln			
	545	550			555
Asn Asp Asn Ala	Pro Glu Ile Leu Tyr	Pro Ala Leu Pro Thr Asp			
	560	565			570
Gly Ser Thr Gly	Val Glu Leu Ala Pro	Arg Ser Ala Glu Pro Gly			
	575	580			585

Tyr	Leu	Val	Thr	Lys	Val	Val	Ala	Val	Asp	Arg	Asp	Ser	Gly	Gln	
				590					595					600	
Asn	Ala	Trp	Leu	Ser	Tyr	Arg	Leu	Leu	Lys	Ala	Ser	Glu	Pro	Gly	
				605					610					615	
Leu	Phe	Ser	Val	Gly	Leu	His	Thr	Gly	Glu	Val	Arg	Thr	Ala	Arg	
				620					625					630	
Ala	Leu	Leu	Asp	Arg	Asp	Ala	Leu	Lys	Gln	Ser	Leu	Val	Val	Ala	
				635					640					645	
Val	Gln	Asp	His	Gly	Gln	Pro	Pro	Leu	Ser	Ala	Thr	Val	Thr	Leu	
				650					655					660	
Thr	Val	Ala	Val	Ala	Asp	Ser	Ile	Pro	Gln	Val	Leu	Ala	Asp	Leu	
				665					670					675	
Gly	Ser	Leu	Glu	Ser	Pro	Ala	Asn	Ser	Glu	Thr	Ser	Asp	Leu	Thr	
				680					685					690	
Leu	Tyr	Leu	Val	Val	Ala	Val	Ala	Ala	Val	Ser	Cys	Val	Phe	Leu	
				695					700					705	
Ala	Phe	Val	Ile	Leu	Leu	Leu	Ala	Leu	Arg	Leu	Arg	Arg	Trp	His	
				710					715					720	
Lys	Ser	Arg	Leu	Leu	Gln	Ala	Ser	Gly	Gly	Gly	Leu	Thr	Gly	Ala	
				725					730					735	
Pro	Ala	Ser	His	Phe	Val	Gly	Val	Asp	Gly	Val	Gln	Ala	Phe	Leu	
				740					745					750	
Gln	Thr	Tyr	Ser	His	Glu	Val	Ser	Leu	Thr	Thr	Asp	Ser	Arg	Lys	
				755					760					765	
Ser	His	Leu	Ile	Phe	Pro	Gln	Pro	Asn	Tyr	Ala	Asp	Met	Leu	Val	
				770					775					780	
Ser	Gln	Glu	Ser	Phe	Glu	Lys	Ser	Glu	Pro	Leu	Leu	Leu	Ser	Gly	
				785					790					795	
Asp	Ser	Val	Phe	Ser	Lys	Asp	Ser	His	Gly	Leu	Ile	Glu	Val	Ser	
				800					805					810	
Leu	Tyr	Gln	Ile	Phe	Phe	Leu	Phe	Phe	Phe	Asn	Cys	Ser	Val	Ser	
				815					820					825	
Gln	Ala	Gly	Val	Gln	Arg	Tyr	Asp	His	Ser	Ser	Leu	Arg	Pro	Gln	
				830					835					840	
Thr	Pro	Arg	Leu	Lys	Gln	Leu	Ser	His	Leu	Cys	Leu	Arg	Cys	Asn	
				845					850					855	
Arg	Asp	Tyr	Arg	Cys	Lys	Pro	Pro	Thr	Val	Cys	Leu	Ser	Ile	Tyr	
				860					865					870	
Leu	Ser	Ile	Tyr	Leu	Ser	Ile	Tyr	Leu	Ser	Ile	Tyr	Leu	Leu	Leu	

	875		880		885
Ser Cys Thr Asp	Gly Ser Leu Thr Pro	Val Ile Pro Val Leu Trp			
	890	895	900		
Glu Ala Glu Ala	Gly Gly Ser Pro Glu	Val Gly Ser Leu Arg Pro			
	905	910	915		

Ala

<210> 391

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 391

tccgtctctg tgaaccgccc cac 23

<210> 392

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 392

ctcgggcgca ttgtcgttct ggtc 24

<210> 393

<211> 40

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 393

ccgactgtga aagagaacgc cccagatcca ctgtgtcccc 40

<210> 394

<211> 999

<212> DNA

<213> Homo sapiens

<400> 394

cccaggctct agtgcaggag gagaaggagg aggagcagga ggtggagatt 50

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ggggcctcct ccaactgggtc cgaatcagta ggtgaccccg cccctggatt 150

ctggaagacc tcaccatggg acgccccga cctcgtgcgg ccaagacgtg 200

His	Pro	Cys	Tyr	Asn	Ser	Ser	Asp	Val	Glu	Asp	His	Asn	His	Asp
				110					115					120
Leu	Met	Leu	Leu	Gln	Leu	Arg	Asp	Gln	Ala	Ser	Leu	Gly	Ser	Lys
				125					130					135
Val	Lys	Pro	Ile	Ser	Leu	Ala	Asp	His	Cys	Thr	Gln	Pro	Gly	Gln
				140					145					150
Lys	Cys	Thr	Val	Ser	Gly	Trp	Gly	Thr	Val	Thr	Ser	Pro	Arg	Glu
				155					160					165
Asn	Phe	Pro	Asp	Thr	Leu	Asn	Cys	Ala	Glu	Val	Lys	Ile	Phe	Pro
				170					175					180
Gln	Lys	Lys	Cys	Glu	Asp	Ala	Tyr	Pro	Gly	Gln	Ile	Thr	Asp	Gly
				185					190					195
Met	Val	Cys	Ala	Gly	Ser	Ser	Lys	Gly	Ala	Asp	Thr	Cys	Gln	Gly
				200					205					210
Asp	Ser	Gly	Gly	Pro	Leu	Val	Cys	Asp	Gly	Ala	Leu	Gln	Gly	Ile
				215					220					225
Thr	Ser	Trp	Gly	Ser	Asp	Pro	Cys	Gly	Arg	Ser	Asp	Lys	Pro	Gly
				230					235					240
Val	Tyr	Thr	Asn	Ile	Cys	Arg	Tyr	Leu	Asp	Trp	Ile	Lys	Lys	Ile
				245					250					255
Ile	Gly	Ser	Lys	Gly										
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<210> 396

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 396

cagcctacag aataaagatg gccc 24

<210> 397

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 397

ggtgcaatga tctgccaggc tgat 24

<210> 398

<211> 48

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 398

agaaataacct gtggttcagt ccataccaaa cccctgctac aacagcag 48

<210> 399

<211> 2236

<212> DNA

<213> Homo sapiens

<400> 399

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gccccggccc gccgcgccgc ccacgcccc accccggccc gcgcccccta 100
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cgccgcgagg ccccgccccg gcccgcccc gcccgcccc ggccggcggg 200
ggaaccgggc ggattcctcg cgcgtcaaac cacctgatcc cataaaacat 250
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 agagcgtgct cagcagccag gtgtgtgtac atacggggtc tctctccacg 2000
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 ttacaggggt cggcggcagc gtttggtcca gaacgccgcc tcccaccag 2150
 atcgcggtat atagagatat gcattttatt ttacttgtgt aaaaatatcg 2200
 gacgacgtgg aataaagagc tcttttctta aaaaaa 2236

<210> 400

<211> 473

<212> PRT

<213> Homo sapiens

<400> 400

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Leu	Trp	Leu	Gln	Ala	Trp	Gln	Val	Ala	Ala	Pro	Cys	Pro	Gly	Ala
			20					25					30	

Cys	Val	Cys	Tyr	Asn	Glu	Pro	Lys	Val	Thr	Thr	Ser	Cys	Pro	Gln	
				35					40					45	
Gln	Gly	Leu	Gln	Ala	Val	Pro	Val	Gly	Ile	Pro	Ala	Ala	Ser	Gln	
				50					55					60	
Arg	Ile	Phe	Leu	His	Gly	Asn	Arg	Ile	Ser	His	Val	Pro	Ala	Ala	
				65					70					75	
Ser	Phe	Arg	Ala	Cys	Arg	Asn	Leu	Thr	Ile	Leu	Trp	Leu	His	Ser	
				80					85					90	
Asn	Val	Leu	Ala	Arg	Ile	Asp	Ala	Ala	Ala	Phe	Thr	Gly	Leu	Ala	
				95					100					105	
Leu	Leu	Glu	Gln	Leu	Asp	Leu	Ser	Asp	Asn	Ala	Gln	Leu	Arg	Ser	
				110					115					120	
Val	Asp	Pro	Ala	Thr	Phe	His	Gly	Leu	Gly	Arg	Leu	His	Thr	Leu	
				125					130					135	
His	Leu	Asp	Arg	Cys	Gly	Leu	Gln	Glu	Leu	Gly	Pro	Gly	Leu	Phe	
				140					145					150	
Arg	Gly	Leu	Ala	Ala	Leu	Gln	Tyr	Leu	Tyr	Leu	Gln	Asp	Asn	Ala	
				155					160					165	
Leu	Gln	Ala	Leu	Pro	Asp	Asp	Thr	Phe	Arg	Asp	Leu	Gly	Asn	Leu	
				170					175					180	
Thr	His	Leu	Phe	Leu	His	Gly	Asn	Arg	Ile	Ser	Ser	Val	Pro	Glu	
				185					190					195	
Arg	Ala	Phe	Arg	Gly	Leu	His	Ser	Leu	Asp	Arg	Leu	Leu	Leu	His	
				200					205					210	
Gln	Asn	Arg	Val	Ala	His	Val	His	Pro	His	Ala	Phe	Arg	Asp	Leu	
				215					220					225	
Gly	Arg	Leu	Met	Thr	Leu	Tyr	Leu	Phe	Ala	Asn	Asn	Leu	Ser	Ala	
				230					235					240	
Leu	Pro	Thr	Glu	Ala	Leu	Ala	Pro	Leu	Arg	Ala	Leu	Gln	Tyr	Leu	
				245					250					255	
Arg	Leu	Asn	Asp	Asn	Pro	Trp	Val	Cys	Asp	Cys	Arg	Ala	Arg	Pro	
				260					265					270	
Leu	Trp	Ala	Trp	Leu	Gln	Lys	Phe	Arg	Gly	Ser	Ser	Ser	Glu	Val	
				275					280					285	
Pro	Cys	Ser	Leu	Pro	Gln	Arg	Leu	Ala	Gly	Arg	Asp	Leu	Lys	Arg	
				290					295					300	
Leu	Ala	Ala	Asn	Asp	Leu	Gln	Gly	Cys	Ala	Val	Ala	Thr	Gly	Pro	
				305					310					315	
Tyr	His	Pro	Ile	Trp	Thr	Gly	Arg	Ala	Thr	Asp	Glu	Glu	Pro	Leu	

320	325	330
Gly Leu Pro Lys Cys Cys Gln Pro Asp	Ala Ala Asp Lys Ala Ser	
335	340	345
Val Leu Glu Pro Gly Arg Pro Ala Ser	Ala Gly Asn Ala Leu Lys	
350	355	360
Gly Arg Val Pro Pro Gly Asp Ser Pro	Pro Gly Asn Gly Ser Gly	
365	370	375
Pro Arg His Ile Asn Asp Ser Pro Phe	Gly Thr Leu Pro Gly Ser	
380	385	390
Ala Glu Pro Pro Leu Thr Ala Val Arg	Pro Glu Gly Ser Glu Pro	
395	400	405
Pro Gly Phe Pro Thr Ser Gly Pro Arg	Arg Arg Pro Gly Cys Ser	
410	415	420
Arg Lys Asn Arg Thr Arg Ser His Cys	Arg Leu Gly Gln Ala Gly	
425	430	435
Ser Gly Gly Gly Gly Thr Gly Asp Ser	Glu Gly Ser Gly Ala Leu	
440	445	450
Pro Ser Leu Thr Cys Ser Leu Thr Pro	Leu Gly Leu Ala Leu Val	
455	460	465
Leu Trp Thr Val Leu Gly Pro Cys		
470		

<210> 401

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 401

tggtgccct gcagtacctc tacc 24

<210> 402

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 402

ccctgcaggt cattggcagc tagg 24

<210> 403

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 403

aggcactgcc tgatgacacc ttccgcgacc tgggcaacct cacac 45

<210> 404

<211> 2738

<212> DNA

<213> Homo sapiens

<400> 404

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ggagaggact actcactggc atatttctga ggtatctgta gaataaccac 100
agcctcagat actggggact ttacagtccc acagaaccgt cctcccagga 150
agctgaatcc agcaagaaca atggaggcca gcgggaagct catttgcaga 200
caaaggcaag tccttttttc ctttctcctt ttgggcttat ctctggcggg 250
cgcggcggaa cctagaagct attctgtggt ggaggaaact gagggcagct 300
cctttgtcac caatttagca aaggacctgg gtctggagca gaggggaattc 350
tccaggcggg gggttagggt tgtttccaga gggaacaaac tacatttgca 400
gctcaatcag gagaccgcg atttgttgct aaatgagaaa ttggaccgtg 450
aggatctgtg cggtcacaca gagccctgtg tgctacgttt ccaagtgttg 500
ctagagagtc ccttcgagtt ttttcaagct gagctgcaag taatagacat 550
aaacgaccac tctccagtat ttctggacaa acaaatgttg gtgaaagtat 600
cagagagcag tcctcctggg actacgtttc ctctgaagaa tgccgaagac 650
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ttaacactca cagcactgga tgggtggtct ccgcccagat ctggcactgc 850
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gaaaaacttc agtcctatga agtcaatatt gaggcaagag atgctggaac 1150

cttttctgga aaatgcaccg ttctgattca agtgategat gtgaacgacc 1200
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 gcgcctgaaa ctgtggttgc acttttcagt gtttcagatc ttgattcagg 1300
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 agagaaagca gagcggaata caacatcact atcactgtca ctgacttggg 1450
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<210> 405
<211> 798
<212> PRT
<213> Homo sapiens

<400> 405
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Phe Ser Phe Leu Leu Leu Gly Leu Ser Leu Ala Gly Ala Ala Glu
20 25 30
Pro Arg Ser Tyr Ser Val Val Glu Glu Thr Glu Gly Ser Ser Phe
35 40 45
Val Thr Asn Leu Ala Lys Asp Leu Gly Leu Glu Gln Arg Glu Phe
50 55 60
Ser Arg Arg Gly Val Arg Val Val Ser Arg Gly Asn Lys Leu His
65 70 75
Leu Gln Leu Asn Gln Glu Thr Ala Asp Leu Leu Leu Asn Glu Lys
80 85 90
Leu Asp Arg Glu Asp Leu Cys Gly His Thr Glu Pro Cys Val Leu
95 100 105
Arg Phe Gln Val Leu Leu Glu Ser Pro Phe Glu Phe Phe Gln Ala
110 115 120
Glu Leu Gln Val Ile Asp Ile Asn Asp His Ser Pro Val Phe Leu
125 130 135
Asp Lys Gln Met Leu Val Lys Val Ser Glu Ser Ser Pro Pro Gly
140 145 150
Thr Thr Phe Pro Leu Lys Asn Ala Glu Asp Leu Asp Val Gly Gln
155 160 165
Asn Asn Ile Glu Asn Tyr Ile Ile Ser Pro Asn Ser Tyr Phe Arg
170 175 180
Val Leu Thr Arg Lys Arg Ser Asp Gly Arg Lys Tyr Pro Glu Leu
185 190 195
Val Leu Asp Lys Ala Leu Asp Arg Glu Glu Glu Ala Glu Leu Arg
200 205 210
Leu Thr Leu Thr Ala Leu Asp Gly Gly Ser Pro Pro Arg Ser Gly
215 220 225
Thr Ala Gln Val Tyr Ile Glu Val Leu Asp Val Asn Asp Asn Ala

230	235	240
Pro Glu Phe Glu Gln Pro Phe Tyr Arg	Val Gln Ile Ser Glu Asp	
245	250	255
Ser Pro Val Gly Phe Leu Val Val Lys	Val Ser Ala Thr Asp Val	
260	265	270
Asp Thr Gly Val Asn Gly Glu Ile Ser	Tyr Ser Leu Phe Gln Ala	
275	280	285
Ser Glu Glu Ile Gly Lys Thr Phe Lys	Ile Asn Pro Leu Thr Gly	
290	295	300
Glu Ile Glu Leu Lys Lys Gln Leu Asp	Phe Glu Lys Leu Gln Ser	
305	310	315
Tyr Glu Val Asn Ile Glu Ala Arg Asp	Ala Gly Thr Phe Ser Gly	
320	325	330
Lys Cys Thr Val Leu Ile Gln Val Ile	Asp Val Asn Asp His Ala	
335	340	345
Pro Glu Val Thr Met Ser Ala Phe Thr	Ser Pro Ile Pro Glu Asn	
350	355	360
Ala Pro Glu Thr Val Val Ala Leu Phe	Ser Val Ser Asp Leu Asp	
365	370	375
Ser Gly Glu Asn Gly Lys Ile Ser Cys	Ser Ile Gln Glu Asp Leu	
380	385	390
Pro Phe Leu Leu Lys Ser Ala Glu Asn	Phe Tyr Thr Leu Leu Thr	
395	400	405
Glu Arg Pro Leu Asp Arg Glu Ser Arg	Ala Glu Tyr Asn Ile Thr	
410	415	420
Ile Thr Val Thr Asp Leu Gly Thr Pro	Met Leu Ile Thr Gln Leu	
425	430	435
Asn Met Thr Val Leu Ile Ala Asp Val	Asn Asp Asn Ala Pro Ala	
440	445	450
Phe Thr Gln Thr Ser Tyr Thr Leu Phe	Val Arg Glu Asn Asn Ser	
455	460	465
Pro Ala Leu His Ile Arg Ser Val Ser	Ala Thr Asp Arg Asp Ser	
470	475	480
Gly Thr Asn Ala Gln Val Thr Tyr Ser	Leu Leu Pro Pro Gln Asp	
485	490	495
Pro His Leu Pro Leu Thr Ser Leu Val	Ser Ile Asn Ala Asp Asn	
500	505	510
Gly His Leu Phe Ala Leu Arg Ser Leu	Asp Tyr Glu Ala Leu Gln	
515	520	525

Gly	Phe	Gln	Phe	Arg	Val	Gly	Ala	Ser	Asp	His	Gly	Ser	Pro	Ala	
				530					535					540	
Leu	Ser	Ser	Glu	Ala	Leu	Val	Arg	Val	Val	Val	Leu	Asp	Ala	Asn	
				545					550					555	
Asp	Asn	Ser	Pro	Phe	Val	Leu	Tyr	Pro	Leu	Gln	Asn	Gly	Ser	Ala	
				560					565					570	
Pro	Cys	Thr	Glu	Leu	Val	Pro	Arg	Ala	Ala	Glu	Pro	Gly	Tyr	Leu	
				575					580					585	
Val	Thr	Lys	Val	Val	Ala	Val	Asp	Gly	Asp	Ser	Gly	Gln	Asn	Ala	
				590					595					600	
Trp	Leu	Ser	Tyr	Gln	Leu	Leu	Lys	Ala	Thr	Glu	Leu	Gly	Leu	Phe	
				605					610					615	
Gly	Val	Trp	Ala	His	Asn	Gly	Glu	Val	Arg	Thr	Ala	Arg	Leu	Leu	
				620					625					630	
Ser	Glu	Arg	Asp	Ala	Ala	Lys	His	Arg	Leu	Val	Val	Leu	Val	Lys	
				635					640					645	
Asp	Asn	Gly	Glu	Pro	Pro	Arg	Ser	Ala	Thr	Ala	Thr	Leu	His	Val	
				650					655					660	
Leu	Leu	Val	Asp	Gly	Phe	Ser	Gln	Pro	Tyr	Leu	Pro	Leu	Pro	Glu	
				665					670					675	
Ala	Ala	Pro	Thr	Gln	Ala	Gln	Ala	Asp	Leu	Leu	Thr	Val	Tyr	Leu	
				680					685					690	
Val	Val	Ala	Leu	Ala	Ser	Val	Ser	Ser	Leu	Phe	Leu	Phe	Ser	Val	
				695					700					705	
Leu	Leu	Phe	Val	Ala	Val	Arg	Leu	Cys	Arg	Arg	Ser	Arg	Ala	Ala	
				710					715					720	
Ser	Val	Gly	Arg	Cys	Leu	Val	Pro	Glu	Gly	Pro	Leu	Pro	Gly	His	
				725					730					735	
Leu	Val	Asp	Met	Ser	Gly	Thr	Arg	Thr	Leu	Ser	Gln	Ser	Tyr	Gln	
				740					745					750	
Tyr	Glu	Val	Cys	Leu	Ala	Gly	Gly	Ser	Gly	Thr	Asn	Glu	Phe	Lys	
				755					760					765	
Phe	Leu	Lys	Pro	Ile	Ile	Pro	Asn	Phe	Pro	Pro	Gln	Cys	Pro	Gly	
				770					775					780	
Lys	Glu	Ile	Gln	Gly	Asn	Ser	Thr	Phe	Pro	Asn	Asn	Phe	Gly	Phe	
				785					790					795	
Asn	Ile	Gln													

<210> 406

<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 406
ctgagaacgc gcctgaaact gtg 23

<210> 407
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 407
agcgttgtca ttgacatcgg cg 22

<210> 408
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 408
ttagttgctc cattcaggag gatctaccct tcctcctgaa atccgcggaa 50

<210> 409
<211> 1379
<212> DNA
<213> Homo sapiens

<400> 409
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gcgtagccgt gcgccgattg cctctcggcc tgggcaatgg tcccggtgc 100
cggtcgacga ccgccccgcg tcatgcggct cctcggctgg tggcaagtat 150
tgctgtgggt gctgggactt cccgtccgcg gcgtggaggt tgcagaggaa 200
agtggtcgct tatggtcaga ggagcagcct gtcaccctc tccaggtggg 250
ggctgtgtac ctgggtgagg aggagtcct gcatgacccg atgggccagg 300
acagggcagc agaagaggcc aatgcggtgc tggggctgga caccgaaggc 350
gatcacatgg tgatgctgtc tgtgattcct ggggaagctg aggacaaagt 400
gagttcagag cctagcggcg tcacctgtgg tgctggagga gcggaggact 450
caaggtgcaa cgtccgagag agccttttct ctctggatgg cgctggagca 500

cacttcctg acagagaaga ggagtattac acagagccag aagtggcgga 550
 atctgacgca gccccgacag aggactccaa taactgaa agtctgaaat 600
 ccccaaaggt gaactgtgag gagagaaaca ttacaggatt agaaaatttc 650
 actctgaaaa ttttaaataat gtcacaggac cttatggatt ttctgaaccc 700
 aaacggtagt gactgtactc tagtcctgtt ttacaccccg tggtgccgct 750
 tttctgccag tttggcccct cactttaact ctctgccccg ggcatttcca 800
 gctcttcact ttttggcact ggatgcatct cagcacagca gcctttctac 850
 caggtttggc accgtagctg ttcctaataat tttattattt caaggagcta 900
 aaccaatggc cagatttaat catacagatc gaacactgga aacactgaaa 950
 atcttcattt ttaatcagac aggtatagaa gccaagaaga atgtggtggt 1000
 aactcaagcc gaccaaataag gccctcttc cagcactttg ataaaaagtg 1050
 tggactgggt gcttgtattt tccttattct ttttaattag ttttattatg 1100
 tatgctacca ttcgaactga gagtattcgg tggctaattc caggacaaga 1150
 gcaggaacat gtggagtagt gatggtctga aagaagttgg aaagaggaac 1200
 ttcaatcctt cgtttcagaa attagtgcta cagtttcata cattttctcc 1250
 agtgacgtgt tgacttgaac cttcaggcag attaaaagaa tcatttggtg 1300
 aacaactgaa tgtataaaaa aattataaac tgggtgttta actagtattg 1350
 caataagcaa atgcaaaaat attcaatag 1379

<210> 410
 <211> 360
 <212> PRT
 <213> Homo sapiens

<400> 410
 Met Val Pro Ala Ala Gly Arg Arg Pro Pro Arg Val Met Arg Leu
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 Leu Gly Trp Trp Gln Val Leu Leu Trp Val Leu Gly Leu Pro Val
 20 25 30
 Arg Gly Val Glu Val Ala Glu Glu Ser Gly Arg Leu Trp Ser Glu
 35 40 45
 Glu Gln Pro Ala His Pro Leu Gln Val Gly Ala Val Tyr Leu Gly
 50 55 60
 Glu Glu Glu Leu Leu His Asp Pro Met Gly Gln Asp Arg Ala Ala
 65 70 75
 Glu Glu Ala Asn Ala Val Leu Gly Leu Asp Thr Gln Gly Asp His

80					85					90				
Met	Val	Met	Leu	Ser	Val	Ile	Pro	Gly	Glu	Ala	Glu	Asp	Lys	Val
				95					100					105
Ser	Ser	Glu	Pro	Ser	Gly	Val	Thr	Cys	Gly	Ala	Gly	Gly	Ala	Glu
				110					115					120
Asp	Ser	Arg	Cys	Asn	Val	Arg	Glu	Ser	Leu	Phe	Ser	Leu	Asp	Gly
				125					130					135
Ala	Gly	Ala	His	Phe	Pro	Asp	Arg	Glu	Glu	Glu	Tyr	Tyr	Thr	Glu
				140					145					150
Pro	Glu	Val	Ala	Glu	Ser	Asp	Ala	Ala	Pro	Thr	Glu	Asp	Ser	Asn
				155					160					165
Asn	Thr	Glu	Ser	Leu	Lys	Ser	Pro	Lys	Val	Asn	Cys	Glu	Glu	Arg
				170					175					180
Asn	Ile	Thr	Gly	Leu	Glu	Asn	Phe	Thr	Leu	Lys	Ile	Leu	Asn	Met
				185					190					195
Ser	Gln	Asp	Leu	Met	Asp	Phe	Leu	Asn	Pro	Asn	Gly	Ser	Asp	Cys
				200					205					210
Thr	Leu	Val	Leu	Phe	Tyr	Thr	Pro	Trp	Cys	Arg	Phe	Ser	Ala	Ser
				215					220					225
Leu	Ala	Pro	His	Phe	Asn	Ser	Leu	Pro	Arg	Ala	Phe	Pro	Ala	Leu
				230					235					240
His	Phe	Leu	Ala	Leu	Asp	Ala	Ser	Gln	His	Ser	Ser	Leu	Ser	Thr
				245					250					255
Arg	Phe	Gly	Thr	Val	Ala	Val	Pro	Asn	Ile	Leu	Leu	Phe	Gln	Gly
				260					265					270
Ala	Lys	Pro	Met	Ala	Arg	Phe	Asn	His	Thr	Asp	Arg	Thr	Leu	Glu
				275					280					285
Thr	Leu	Lys	Ile	Phe	Ile	Phe	Asn	Gln	Thr	Gly	Ile	Glu	Ala	Lys
				290					295					300
Lys	Asn	Val	Val	Val	Thr	Gln	Ala	Asp	Gln	Ile	Gly	Pro	Leu	Pro
				305					310					315
Ser	Thr	Leu	Ile	Lys	Ser	Val	Asp	Trp	Leu	Leu	Val	Phe	Ser	Leu
				320					325					330
Phe	Phe	Leu	Ile	Ser	Phe	Ile	Met	Tyr	Ala	Thr	Ile	Arg	Thr	Glu
				335					340					345
Ser	Ile	Arg	Trp	Leu	Ile	Pro	Gly	Gln	Glu	Gln	Glu	His	Val	Glu
				350					355					360

<210> 411
 <211> 24

aaggtatgtg aagcctgcaa aaataaaaat gatgatgaca acgacataat 600
 ggaaacgctt tgtaaaaatg attttgcact gaaaataaaa gtgaaggaga 650
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 accatttaca agctgaacgg tgtgtccgaa agggacctga agaaatcggg 750
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 tcaacgcgcc ctatctggtc atgggacaga aacaggggtg ggagctggtg 850
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 gaatcttgta gaaatattca aactaataaa atcatgaata ttttaa 1196

<210> 415

<211> 295

<212> PRT

<213> Homo sapiens

<400> 415

Met	Leu	Gln	Gly	Pro	Gly	Ser	Leu	Leu	Leu	Leu	Phe	Leu	Ala	Ser
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His	Cys	Cys	Leu	Gly	Ser	Ala	Arg	Gly	Leu	Phe	Leu	Phe	Gly	Gln
			20						25					30
Pro	Asp	Phe	Ser	Tyr	Lys	Arg	Ser	Asn	Cys	Lys	Pro	Ile	Pro	Val
			35						40					45
Asn	Leu	Gln	Leu	Cys	His	Gly	Ile	Glu	Tyr	Gln	Asn	Met	Arg	Leu
			50						55					60
Pro	Asn	Leu	Leu	Gly	His	Glu	Thr	Met	Lys	Glu	Val	Leu	Glu	Gln
			65						70					75
Ala	Gly	Ala	Trp	Ile	Pro	Leu	Val	Met	Lys	Gln	Cys	His	Pro	Asp
			80						85					90
Thr	Lys	Lys	Phe	Leu	Cys	Ser	Leu	Phe	Ala	Pro	Val	Cys	Leu	Asp
			95						100					105
Asp	Leu	Asp	Glu	Thr	Ile	Gln	Pro	Cys	His	Ser	Leu	Cys	Val	Gln
			110						115					120
Val	Lys	Asp	Arg	Cys	Ala	Pro	Val	Met	Ser	Ala	Phe	Gly	Phe	Pro
			125						130					135

Trp	Pro	Asp	Met	Leu	Glu	Cys	Asp	Arg	Phe	Pro	Gln	Asp	Asn	Asp	
				140					145					150	
Leu	Cys	Ile	Pro	Leu	Ala	Ser	Ser	Asp	His	Leu	Leu	Pro	Ala	Thr	
				155					160					165	
Glu	Glu	Ala	Pro	Lys	Val	Cys	Glu	Ala	Cys	Lys	Asn	Lys	Asn	Asp	
				170					175					180	
Asp	Asp	Asn	Asp	Ile	Met	Glu	Thr	Leu	Cys	Lys	Asn	Asp	Phe	Ala	
				185					190					195	
Leu	Lys	Ile	Lys	Val	Lys	Glu	Ile	Thr	Tyr	Ile	Asn	Arg	Asp	Thr	
				200					205					210	
Lys	Ile	Ile	Leu	Glu	Thr	Lys	Ser	Lys	Thr	Ile	Tyr	Lys	Leu	Asn	
				215					220					225	
Gly	Val	Ser	Glu	Arg	Asp	Leu	Lys	Lys	Ser	Val	Leu	Trp	Leu	Lys	
				230					235					240	
Asp	Ser	Leu	Gln	Cys	Thr	Cys	Glu	Glu	Met	Asn	Asp	Ile	Asn	Ala	
				245					250					255	
Pro	Tyr	Leu	Val	Met	Gly	Gln	Lys	Gln	Gly	Gly	Glu	Leu	Val	Ile	
				260					265					270	
Thr	Ser	Val	Lys	Arg	Trp	Gln	Lys	Gly	Gln	Arg	Glu	Phe	Lys	Arg	
				275					280					285	
Ile	Ser	Arg	Ser	Ile	Arg	Lys	Leu	Gln	Cys						
				290					295						

<210> 416
 <211> 21
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 416
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<210> 417
 <211> 25
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 417
 cctcacaggt gcaactgcaag ctgtc 25

<210> 418
 <211> 47
 <212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 418

ctcttcctct ttggccagcc cgacttctcc tacaagcgca gaattgc 47

<210> 419

<211> 1830

<212> DNA

<213> Homo sapiens

<400> 419

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gctgtggctc agctttgcac ctgtggctga cgtcattgct gaggacttgg 200
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tggagttggc ggtcgagtgt tccttccccg tgggggaggg ggctgccaca 1150
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 <212> PRT
 <213> Homo sapiens

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 35 40 45
 Leu Trp Leu Ser Phe Ala Pro Val Ala Asp Val Ile Ala Glu Asp
 50 55 60
 Leu Val Leu Ser Met Glu Gln Ile Asn Trp Leu Ser Leu Val Tyr
 65 70 75
 Leu Val Val Ser Thr Pro Phe Gly Val Ala Ala Ile Trp Ile Leu
 80 85 90
 Asp Ser Val Gly Leu Arg Ala Ala Thr Ile Leu Gly Ala Trp Leu
 95 100 105
 Asn Phe Ala Gly Ser Val Leu Arg Met Val Pro Cys Met Val Val

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Gly	Thr	Gln	Asn	Pro 125	Phe	Ala	Phe	Leu	Met 130	Gly	Gly	Gln	Ser	Leu 135
Cys	Ala	Leu	Ala	Gln 140	Ser	Leu	Val	Ile	Phe 145	Ser	Pro	Ala	Lys	Leu 150
Ala	Ala	Leu	Trp	Phe 155	Pro	Glu	His	Gln	Arg 160	Ala	Thr	Ala	Asn	Met 165
Leu	Ala	Thr	Met	Ser 170	Asn	Pro	Leu	Gly	Val 175	Leu	Val	Ala	Asn	Val 180
Leu	Ser	Pro	Val	Leu 185	Val	Lys	Lys	Gly	Glu 190	Asp	Ile	Pro	Leu	Met 195
Leu	Gly	Val	Tyr	Thr 200	Ile	Pro	Ala	Gly	Val 205	Val	Cys	Leu	Leu	Ser 210
Thr	Ile	Cys	Leu	Trp 215	Glu	Ser	Val	Pro	Pro 220	Thr	Pro	Pro	Ser	Ala 225
Gly	Ala	Ala	Ser	Ser 230	Thr	Ser	Glu	Lys	Phe 235	Leu	Asp	Gly	Leu	Lys 240
Leu	Gln	Leu	Met	Trp 245	Asn	Lys	Ala	Tyr	Val 250	Ile	Leu	Ala	Val	Cys 255
Leu	Gly	Gly	Met	Ile 260	Gly	Ile	Ser	Ala	Ser 265	Phe	Ser	Ala	Leu	Leu 270
Glu	Gln	Ile	Leu	Cys 275	Ala	Ser	Gly	His	Ser 280	Ser	Gly	Phe	Ser	Gly 285
Leu	Cys	Gly	Ala	Leu 290	Phe	Ile	Thr	Phe	Gly 295	Ile	Leu	Gly	Ala	Leu 300
Ala	Leu	Gly	Pro	Tyr 305	Val	Asp	Arg	Thr	Lys 310	His	Phe	Thr	Glu	Ala 315
Thr	Lys	Ile	Gly	Leu 320	Cys	Leu	Phe	Ser	Leu 325	Ala	Cys	Val	Pro	Phe 330
Ala	Leu	Val	Ser	Gln 335	Leu	Gln	Gly	Gln	Thr 340	Leu	Ala	Leu	Ala	Ala 345
Thr	Cys	Ser	Leu	Leu 350	Gly	Leu	Phe	Gly	Phe 355	Ser	Val	Gly	Pro	Val 360
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Leu	Ile	Met	Leu	Ala 395	Met	Thr	Ala	Leu	Thr 400	Val	Arg	Arg	Ser	Glu 405

Pro	Ser	Leu	Ser	Thr	Cys	Gln	Gln	Gly	Glu	Asp	Pro	Leu	Asp	Trp
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Thr	Val	Ser	Leu	Leu	Leu	Met	Ala	Gly	Leu	Cys	Thr	Phe	Phe	Ser
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Cys	Ile	Leu	Ala	Val	Phe	Phe	His	Thr	Pro	Tyr	Arg	Arg	Leu	Gln
				440					445					450
Ala	Glu	Ser	Gly	Glu	Pro	Pro	Ser	Thr	Arg	Asn	Ala	Val	Gly	Gly
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Ala	Asp	Ser	Gly	Pro	Gly	Val	Asp	Arg	Gly	Gly	Ala	Gly	Arg	Ala
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Gly	Val	Leu	Gly	Pro	Ser	Thr	Ala	Thr	Pro	Glu	Cys	Thr	Ala	Arg
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Ala	Cys	His	Arg	Ala	Thr	Pro	Arg	Ala	Gln	Gly	Pro	Ala	Ala	Thr
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Asp	Ala	Pro	Ser	Arg	Pro	Gly	Arg	Leu	Ala	Gly	Arg	Val	Gln	Ala
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Ser	Arg	Phe	Ile	Asp	Pro	Ala	Gly	Ser	His	Ser	Ser	Phe	Ser	Ser
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<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 421

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<210> 422

<211> 25

<212> DNA

<213> Artificial Sequence

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<223> Synthetic oligonucleotide probe

<400> 422

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<210> 423

<211> 43

<212> DNA

<213> Artificial Sequence

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<223> Synthetic oligonucleotide probe

<400> 423

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<210> 424

<211> 4313

<212> DNA

<213> Homo sapiens

<400> 424

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 <211> 1184
 <212> PRT
 <213> Homo sapiens

<400> 425
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 Thr Val Lys Tyr Gln Val Ser Glu Glu Val Pro Ser Gly Thr Val
 35 40 45
 Ile Gly Lys Leu Ser Gln Glu Leu Gly Arg Glu Glu Arg Arg Arg
 50 55 60
 Gln Ala Gly Ala Ala Phe Gln Val Leu Gln Leu Pro Gln Ala Leu
 65 70 75
 Pro Ile Gln Val Asp Ser Glu Glu Gly Leu Leu Ser Thr Gly Arg
 80 85 90
 Arg Leu Asp Arg Glu Gln Leu Cys Arg Gln Trp Asp Pro Cys Leu
 95 100 105
 Val Ser Phe Asp Val Leu Ala Thr Gly Asp Leu Ala Leu Ile His
 110 115 120
 Val Glu Ile Gln Val Leu Asp Ile Asn Asp His Gln Pro Arg Phe
 125 130 135
 Pro Lys Gly Glu Gln Glu Leu Glu Ile Ser Glu Ser Ala Ser Leu
 140 145 150
 Arg Thr Arg Ile Pro Leu Asp Arg Ala Leu Asp Pro Asp Thr Gly
 155 160 165
 Pro Asn Thr Leu His Thr Tyr Thr Leu Ser Pro Ser Glu His Phe
 170 175 180
 Ala Leu Asp Val Ile Val Gly Pro Asp Glu Thr Lys His Ala Glu
 185 190 195

Leu	Ile	Val	Val	Lys	Glu	Leu	Asp	Arg	Glu	Ile	His	Ser	Phe	Phe	
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Asp	Leu	Val	Leu	Thr	Ala	Tyr	Asp	Asn	Gly	Asn	Pro	Pro	Lys	Ser	
				215					220					225	
Gly	Thr	Ser	Leu	Val	Lys	Val	Asn	Val	Leu	Asp	Ser	Asn	Asp	Asn	
				230					235					240	
Ser	Pro	Ala	Phe	Ala	Glu	Ser	Ser	Leu	Ala	Leu	Glu	Ile	Gln	Glu	
				245					250					255	
Asp	Ala	Ala	Pro	Gly	Thr	Leu	Leu	Ile	Lys	Leu	Thr	Ala	Thr	Asp	
				260					265					270	
Pro	Asp	Gln	Gly	Pro	Asn	Gly	Glu	Val	Glu	Phe	Phe	Leu	Ser	Lys	
				275					280					285	
His	Met	Pro	Pro	Glu	Val	Leu	Asp	Thr	Phe	Ser	Ile	Asp	Ala	Lys	
				290					295					300	
Thr	Gly	Gln	Val	Ile	Leu	Arg	Arg	Pro	Leu	Asp	Tyr	Glu	Lys	Asn	
				305					310					315	
Pro	Ala	Tyr	Glu	Val	Asp	Val	Gln	Ala	Arg	Asp	Leu	Gly	Pro	Asn	
				320					325					330	
Pro	Ile	Pro	Ala	His	Cys	Lys	Val	Leu	Ile	Lys	Val	Leu	Asp	Val	
				335					340					345	
Asn	Asp	Asn	Ile	Pro	Ser	Ile	His	Val	Thr	Trp	Ala	Ser	Gln	Pro	
				350					355					360	
Ser	Leu	Val	Ser	Glu	Ala	Leu	Pro	Lys	Asp	Ser	Phe	Ile	Ala	Leu	
				365					370					375	
Val	Met	Ala	Asp	Asp	Leu	Asp	Ser	Gly	His	Asn	Gly	Leu	Val	His	
				380					385					390	
Cys	Trp	Leu	Ser	Gln	Glu	Leu	Gly	His	Phe	Arg	Leu	Lys	Arg	Thr	
				395					400					405	
Asn	Gly	Asn	Thr	Tyr	Met	Leu	Leu	Thr	Asn	Ala	Thr	Leu	Asp	Arg	
				410					415					420	
Glu	Gln	Trp	Pro	Lys	Tyr	Thr	Leu	Thr	Leu	Leu	Ala	Gln	Asp	Gln	
				425					430					435	
Gly	Leu	Gln	Pro	Leu	Ser	Ala	Lys	Lys	Gln	Leu	Ser	Ile	Gln	Ile	
				440					445					450	
Ser	Asp	Ile	Asn	Asp	Asn	Ala	Pro	Val	Phe	Glu	Lys	Ser	Arg	Tyr	
				455					460					465	
Glu	Val	Ser	Thr	Arg	Glu	Asn	Asn	Leu	Pro	Ser	Leu	His	Leu	Ile	
				470					475					480	
Thr	Ile	Lys	Ala	His	Asp	Ala	Asp	Leu	Gly	Ile	Asn	Gly	Lys	Val	

	485	490	495
Ser Tyr Arg Ile	Gln Asp Ser Pro Val	Ala His Leu Val	Ala Ile
	500	505	510
Asp Ser Asn Thr	Gly Glu Val Thr Ala	Gln Arg Ser Leu Asn	Tyr
	515	520	525
Glu Glu Met Ala	Gly Phe Glu Phe Gln	Val Ile Ala Glu Asp	Ser
	530	535	540
Gly Gln Pro Met	Leu Ala Ser Ser Val	Ser Val Trp Val Ser	Leu
	545	550	555
Leu Asp Ala Asn	Asp Asn Ala Pro Glu	Val Val Gln Pro Val	Leu
	560	565	570
Ser Asp Gly Lys	Ala Ser Leu Ser Val	Leu Val Asn Ala Ser	Thr
	575	580	585
Gly His Leu Leu	Val Pro Ile Glu Thr	Pro Asn Gly Leu Gly	Pro
	590	595	600
Ala Gly Thr Asp	Thr Pro Pro Leu Ala	Thr His Ser Ser Arg	Pro
	605	610	615
Phe Leu Leu Thr	Thr Ile Val Ala Arg	Asp Ala Asp Ser Gly	Ala
	620	625	630
Asn Gly Glu Pro	Leu Tyr Ser Ile Arg	Asn Gly Asn Glu Ala	His
	635	640	645
Leu Phe Ile Leu	Asn Pro His Thr Gly	Gln Leu Phe Val Asn	Val
	650	655	660
Thr Asn Ala Ser	Ser Leu Ile Gly Ser	Glu Trp Glu Leu Glu	Ile
	665	670	675
Val Val Glu Asp	Gln Gly Ser Pro Pro	Leu Gln Thr Arg Ala	Leu
	680	685	690
Leu Arg Val Met	Phe Val Thr Ser Val	Asp His Leu Arg Asp	Ser
	695	700	705
Ala Arg Lys Pro	Gly Ala Leu Ser Met	Ser Met Leu Thr Val	Ile
	710	715	720
Cys Leu Ala Val	Leu Leu Gly Ile Phe	Gly Leu Ile Leu Ala	Leu
	725	730	735
Phe Met Ser Ile	Cys Arg Thr Glu Lys	Lys Asp Asn Arg Ala	Tyr
	740	745	750
Asn Cys Arg Glu	Ala Glu Ser Thr Tyr	Arg Gln Gln Pro Lys	Arg
	755	760	765
Pro Gln Lys His	Ile Gln Lys Ala Asp	Ile His Leu Val Pro	Val
	770	775	780

Leu	Arg	Gly	Gln	Ala	Gly	Glu	Pro	Cys	Glu	Val	Gly	Gln	Ser	His	
				785					790					795	
Lys	Asp	Val	Asp	Lys	Glu	Ala	Met	Met	Glu	Ala	Gly	Trp	Asp	Pro	
				800					805					810	
Cys	Leu	Gln	Ala	Pro	Phe	His	Leu	Thr	Pro	Thr	Leu	Tyr	Arg	Thr	
				815					820					825	
Leu	Arg	Asn	Gln	Gly	Asn	Gln	Gly	Ala	Pro	Ala	Glu	Ser	Arg	Glu	
				830					835					840	
Val	Leu	Gln	Asp	Thr	Val	Asn	Leu	Leu	Phe	Asn	His	Pro	Arg	Gln	
				845					850					855	
Arg	Asn	Ala	Ser	Arg	Glu	Asn	Leu	Asn	Leu	Pro	Glu	Pro	Gln	Pro	
				860					865					870	
Ala	Thr	Gly	Gln	Pro	Arg	Ser	Arg	Pro	Leu	Lys	Val	Ala	Gly	Ser	
				875					880					885	
Pro	Thr	Gly	Arg	Leu	Ala	Gly	Asp	Gln	Gly	Ser	Glu	Glu	Ala	Pro	
				890					895					900	
Gln	Arg	Pro	Pro	Ala	Ser	Ser	Ala	Thr	Leu	Arg	Arg	Gln	Arg	His	
				905					910					915	
Leu	Asn	Gly	Lys	Val	Ser	Pro	Glu	Lys	Glu	Ser	Gly	Pro	Arg	Gln	
				920					925					930	
Ile	Leu	Arg	Ser	Leu	Val	Arg	Leu	Ser	Val	Ala	Ala	Phe	Ala	Glu	
				935					940					945	
Arg	Asn	Pro	Val	Glu	Glu	Leu	Thr	Val	Asp	Ser	Pro	Pro	Val	Gln	
				950					955					960	
Gln	Ile	Ser	Gln	Leu	Leu	Ser	Leu	Leu	His	Gln	Gly	Gln	Phe	Gln	
				965					970					975	
Pro	Lys	Pro	Asn	His	Arg	Gly	Asn	Lys	Tyr	Leu	Ala	Lys	Pro	Gly	
				980					985					990	
Gly	Ser	Arg	Ser	Ala	Ile	Pro	Asp	Thr	Asp	Gly	Pro	Ser	Ala	Arg	
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Ala	Gly	Gly	Gln	Thr	Asp	Pro	Glu	Gln	Glu	Glu	Gly	Pro	Leu	Asp	
				1010					1015					1020	
Pro	Glu	Glu	Asp	Leu	Ser	Val	Lys	Gln	Leu	Leu	Glu	Glu	Glu	Leu	
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Ser	Ser	Leu	Leu	Asp	Pro	Ser	Thr	Gly	Leu	Ala	Leu	Asp	Arg	Leu	
				1040					1045					1050	
Ser	Ala	Pro	Asp	Pro	Ala	Trp	Met	Ala	Arg	Leu	Ser	Leu	Pro	Leu	
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Thr	Thr	Asn	Tyr	Arg	Asp	Asn	Val	Ile	Ser	Pro	Asp	Ala	Ala	Ala	

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Pro Glu Leu Ser Pro Thr Gly Thr Arg Leu Ala Ser Thr Phe Val		
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Ser Glu Met Ser Ser Leu Leu Glu Met Leu Leu Glu Gln Arg Ser		
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Ser Met Pro Val Glu Ala Ala Ser Glu Ala Leu Arg Arg Leu Ser		
1130	1135	1140
Val Cys Gly Arg Thr Leu Ser Leu Asp Leu Ala Thr Ser Ala Ala		
1145	1150	1155
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1175	1180	

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 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 426
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<210> 427
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 427
 gtgacgtgga tgcttggtgat gttg 24

<210> 428
 <211> 50
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 428
 tggacacctt cagtattgat gccaaagacag gccaggtcat tctgcgtcga 50

<210> 429
 <211> 2037

<212> DNA
<213> Homo sapiens

<400> 429

cggaacgcgtg ggcggacgcg tgggggagag ccgcagtcgc ggctgcagca 50
cctggggagaa ggcagaccgt gtgagggggc ctgtggcccc agcgtgctgt 100
ggcctcgggg agtggaagt ggaggcagga gccttcctta cacttcgcca 150
tgagtttcct catcgactcc agcatcatga ttacctocca gatactattt 200
tttggatttg ggtggctttt cttcatgcgc caattgttta aagactatga 250
gatacgtcag tatgttgtag aggtgatctt ctccgtgacg tttgcatttt 300
cttgacccat gtttgagctc atcatctttg aaatcttagg agtattgaat 350
agcagctccc gttattttca ctggaaaatg aacctgtgtg taattctgct 400
gatcctgggt ttcattggtc ctttttacct tggctatttt attgtgagca 450
atatccgact actgcataaa caacgactgc ttttttcctg tctcttatgg 500
ctgaccttta tgtatttctt ctggaaacta ggagatccct tccccattct 550
cagcccaaaa catgggatct tatccataga acagctcatc agccgggttg 600
gtgtgattgg agtgactctc atggctcttc tttctggatt tgggtgctgtc 650
aactgcccac acacttacat gtcttacttc ctcaggaatg tgactgacac 700
ggatattcta gccctggaac ggcgactgct gcaaaccatg gatatgatca 750
taagcaaaaa gaaaaggatg gcaatggcac ggagaacaat gttccagaag 800
ggggaagtgc ataacaacc atcaggtttc tggggaatga taaaaagtgt 850
taccattca gcatcaggaa gtgaaaatct tactcttatt caacaggaag 900
tggatgcttt ggaagaatta agcaggcagc tttttctgga aacagctgat 950
ctatatgcta ccaaggagag aatagaatac tccaaaacct tcaaggggaa 1000
atattttaat tttcttggtt actttttctc tattttactgt gtttggaaaa 1050
ttttcatggc taccatcaat attgtttttg atcgagttgg gaaaacggat 1100
cctgtcacia gaggcattga gatcactgtg aattatctgg gaatccaatt 1150
tgatgtgaag ttttggctcc aacacatttc cttcattctt gttggaataa 1200
tcacgtcac atccatcaga ggattgctga tcaactctac caagttcttt 1250
tatgccatct ctagcagtaa gtctccaat gtcattgtcc tgctattaga 1300
acagataatg ggcatgtact ttgtctctc tgtgctgctg atccgaatga 1350

gtatgccttt agaataccgc accataatca ctgaagtcct tggagaactg 1400
cagttcaact tctatcaccg ttggtttgat gtgatcttcc tggtcagcgc 1450
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agcaaattggc accttgaact taagcctact acagactggt agaggccagt 1550
ggttttcaaaa tttagatata agagggggga aaaatggaac cagggcctga 1600
cattttataa acaaacaaaa tgctatggta gcatttttca cttcatagc 1650
atactccttc cccgtcaggt gatactatga ccatgagtag catcagccag 1700
aacatgagag ggagaactaa ctcaagacaa tactcagcag agagcatccc 1750
gtgtggatat gaggctggtg tagaggcgga gaggagccaa gaaactaaag 1800
gtgaaaaata cactggaact ctggggcaag acatgtctat ggtagctgag 1850
ccaaacacgt aggatttccg ttttaagggt cacatggaaa aggttatagc 1900
tttgccctga gattgactca ttaaaatcag agactgtaac aaaaaaaaaa 1950
aaaaaaaaaa agggcgggccg cgactctaga gtcgacctgc agaagcttgg 2000
ccgccatggc ccaacttggt tattgcagct tataatg 2037

<210> 430
<211> 455
<212> PRT
<213> Homo sapiens

<400> 430
Met Ser Phe Leu Ile Asp Ser Ser Ile Met Ile Thr Ser Gln Ile
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Leu Phe Phe Gly Phe Gly Trp Leu Phe Phe Met Arg Gln Leu Phe
20 25 30
Lys Asp Tyr Glu Ile Arg Gln Tyr Val Val Gln Val Ile Phe Ser
35 40 45
Val Thr Phe Ala Phe Ser Cys Thr Met Phe Glu Leu Ile Ile Phe
50 55 60
Glu Ile Leu Gly Val Leu Asn Ser Ser Ser Arg Tyr Phe His Trp
65 70 75
Lys Met Asn Leu Cys Val Ile Leu Leu Ile Leu Val Phe Met Val
80 85 90
Pro Phe Tyr Ile Gly Tyr Phe Ile Val Ser Asn Ile Arg Leu Leu
95 100 105
His Lys Gln Arg Leu Leu Phe Ser Cys Leu Leu Trp Leu Thr Phe
110 115 120

Met	Tyr	Phe	Phe	Trp	Lys	Leu	Gly	Asp	Pro	Phe	Pro	Ile	Leu	Ser	
				125					130					135	
Pro	Lys	His	Gly	Ile	Leu	Ser	Ile	Glu	Gln	Leu	Ile	Ser	Arg	Val	
				140					145					150	
Gly	Val	Ile	Gly	Val	Thr	Leu	Met	Ala	Leu	Leu	Ser	Gly	Phe	Gly	
				155					160					165	
Ala	Val	Asn	Cys	Pro	Tyr	Thr	Tyr	Met	Ser	Tyr	Phe	Leu	Arg	Asn	
				170					175					180	
Val	Thr	Asp	Thr	Asp	Ile	Leu	Ala	Leu	Glu	Arg	Arg	Leu	Leu	Gln	
				185					190					195	
Thr	Met	Asp	Met	Ile	Ile	Ser	Lys	Lys	Lys	Arg	Met	Ala	Met	Ala	
				200					205					210	
Arg	Arg	Thr	Met	Phe	Gln	Lys	Gly	Glu	Val	His	Asn	Lys	Pro	Ser	
				215					220					225	
Gly	Phe	Trp	Gly	Met	Ile	Lys	Ser	Val	Thr	Thr	Ser	Ala	Ser	Gly	
				230					235					240	
Ser	Glu	Asn	Leu	Thr	Leu	Ile	Gln	Gln	Glu	Val	Asp	Ala	Leu	Glu	
				245					250					255	
Glu	Leu	Ser	Arg	Gln	Leu	Phe	Leu	Glu	Thr	Ala	Asp	Leu	Tyr	Ala	
				260					265					270	
Thr	Lys	Glu	Arg	Ile	Glu	Tyr	Ser	Lys	Thr	Phe	Lys	Gly	Lys	Tyr	
				275					280					285	
Phe	Asn	Phe	Leu	Gly	Tyr	Phe	Phe	Ser	Ile	Tyr	Cys	Val	Trp	Lys	
				290					295					300	
Ile	Phe	Met	Ala	Thr	Ile	Asn	Ile	Val	Phe	Asp	Arg	Val	Gly	Lys	
				305					310					315	
Thr	Asp	Pro	Val	Thr	Arg	Gly	Ile	Glu	Ile	Thr	Val	Asn	Tyr	Leu	
				320					325					330	
Gly	Ile	Gln	Phe	Asp	Val	Lys	Phe	Trp	Ser	Gln	His	Ile	Ser	Phe	
				335					340					345	
Ile	Leu	Val	Gly	Ile	Ile	Ile	Val	Thr	Ser	Ile	Arg	Gly	Leu	Leu	
				350					355					360	
Ile	Thr	Leu	Thr	Lys	Phe	Phe	Tyr	Ala	Ile	Ser	Ser	Ser	Lys	Ser	
				365					370					375	
Ser	Asn	Val	Ile	Val	Leu	Leu	Leu	Ala	Gln	Ile	Met	Gly	Met	Tyr	
				380					385					390	
Phe	Val	Ser	Ser	Val	Leu	Leu	Ile	Arg	Met	Ser	Met	Pro	Leu	Glu	
				395					400					405	
Tyr	Arg	Thr	Ile	Ile	Thr	Glu	Val	Leu	Gly	Glu	Leu	Gln	Phe	Asn	

410	415	420
Phe Tyr His Arg Trp Phe Asp Val Ile	Phe Leu Val Ser Ala Leu	
425	430	435
Ser Ser Ile Leu Phe Leu Tyr Leu Ala	His Lys Gln Ala Pro Glu	
440	445	450
Lys Gln Met Ala Pro		
455		

<210> 431
 <211> 407
 <212> DNA
 <213> Homo sapiens

<220>
 <221> unsure
 <222> 78, 81, 113, 157, 224, 297
 <223> unknown base

<400> 431
 catgggaagt ggagccggag ccttccttac actcgccatg agtttctca 50
 tcgactccag catcatgatt acctcccnga nactatTTTT tggatttggg 100
 tggcttttct tcnngcccaa tgtttaaaga ctatgagata cgtcagtatg 150
 ttgtacnggt gatcttctcc gtgacgtttg ccatttcttg caccatgttt 200
 gagctcatca tctttgaaat cttnngagta ttgaatagca gctcccgtta 250
 ttttacttgg aaaatgaacc tgtgtgtaat tctgctgatc ctggttntca 300
 tggtgctttt ttacattggc tattttattg tgagcaatat ccgactactg 350
 cataaacaac gactgctttt ttctgtctc ttatggctga cctttatgta 400
 tttccag 407

<210> 432
 <211> 457
 <212> DNA
 <213> Homo sapiens

<220>
 <221> unsure
 <222> 31, 66, 81-82, 84, 122, 184, 187, 232, 241, 400, 424, 427, 434
 <223> unknown base

<400> 432
 gtgttgcct tggggagggg aaggggagcc nggcccttc ctaaaatttg 50
 gccagggtt tcttnttga attccgggtt nngnatacct tcccagaaaa 100
 tatttttttg atttggggta gnttttttcc atgcgccaat tgtttaaaga 150
 ctatgagata cgtcagtatg ttgtacaggt gatnttntcc gtgacgtttg 200

cattttcttg caccatgttt gagctcatca tntttgaaat nttaggagta 250
 ttgaatagca gctcccgtta ttttcaactgg aaaatgaacc tgtgtgtaat 300
 tctgctgac ctggttttca tgggtgccttt ttacattggc tattttattg 350
 tgagcaatat ccgactactg cataaacaac gactgctttt ttctgtctn 400
 ttatggctga cctttatgta tttnttntgg aaantaggag atccctttcc 450
 cattctc 457

<210> 433
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 433
 aagtggagcc ggagccttcc 20

<210> 434
 <211> 22
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 434
 tcgttggtta tgcagtagtc gg 22

<210> 435
 <211> 41
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 435
 attgtttaaa gactatgaga tacgtcagta tggtgtacag g 41

<210> 436
 <211> 3951
 <212> DNA
 <213> Homo sapiens

<400> 436
 ctgcgcagc gatcgccca tggccggggc tcggagccgc gacccttggg 50
 gggcctccgg gatttgctac ctttttggct cctgtctgt cgaactgtc 100
 ttctcacggg ctgtgcctt caatctggac gtgatgggtg ccttgcgcaa 150
 ggagggcgag ccaggcagcc tcttcggctt ctctgtggcc ctgcaccggc 200

agttgcagcc ccgacccccag agctggctgc tgggtgggtgc tccccaggcc 250
 ctggctcttc ctgggcagca ggcgaatcgc actggaggcc tcttcgcttg 300
 cccgttgagc ctggaggaga ctgactgcta cagagtggac atcgaccagg 350
 gagctgatat gcaaaaggaa agcaaggaga accagtgggtt gggagtcaat 400
 gttcggagcc aggggccttg gggcaagatt gttacctgtg cacaccgata 450
 tgaggcaagg cagcgagtgg accagatcct ggagacgagg gatatgattg 500
 gtcgctgctt tgtgctcagc caggacctgg ccatccggga tgagttggat 550
 ggtgggggaat ggaagttctg tgagggacgc cccaaggcc atgaacaatt 600
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 gtggagctct gtgcacaggg ctacagcggac ctggcacacc tggacgacgg 750
 tccctacgag gcggggggag agaaggagca ggacccccgc ctcatcccg 800
 tccctgccaa cagctacttt ggcttctcta ttgactcggg gaaaggtctg 850
 gtgcgtgcag aagagctgag ctttgtggct ggagcccccc gcgccaacca 900
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 tgtacttgaa ccaggggggt cactgggctg ggatctcccc tctccggctc 1150
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 aaaccttcac aggtgctgga gggcgaggct gtgggcatca agagcttcgg 1350
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 tgctgggtgg ctccctggct gacaccgag tgctcttcag ggccagaccc 1450
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 ctggactatg tgtagatgc ggacacagac cggaggctcc ggggccagg 1650

tccccgtgtg acgttctctga gccgtaacct ggaagaacct aagcaccagg 1700
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 gccatgttcc agctccagga aaatgtcaaa gacaagcttc gggccattgt 1800
 agtgaccttg tctacagtc tccagacccc tcggctccgg cgacaggctc 1850
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 ggtcaccaac ctgccatcgg acccagccca gcccaggct gatggggatg 2150
 atgcccatag agcccagctc ctggctatgc ttctgactc actgcactac 2200
 tcaggggtcc gggccctgga cctgcggag aagccactct gcctgtccaa 2250
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 gtgcccaggc caccttctac ctcatcctta gcacctccgg gatcagcatt 2350
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 gtgaggggag agagagccat gcagtctgag cgggatgtgg gcagcaaggc 2550
 caagtatgag gtcacggttt ccaaccaagg ccagtcgctc agaaccctgg 2600
 gctctgcctt cctcaacatc atgtggcctc atgagattgc caatgggaag 2650
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gtataacttgg accccatggc tgtggtggca gaaggagtgc cctggtgggt 3150
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tgctcctgtg gaagatggga ttcttcaaac gggcgaagca ccccgaggcc 3250
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gtaacaggac cccaaggacc tgcctccccg gaagtgcctt aacctagagg 3800
gtcggggagg aggttgtgtc actgactcag gctgctcctt ctctagtttc 3850
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ttcgtctatt tattaaaaa tatttgagaa caaaaaaaaa aaaaaaaaaa 3950
a 3951

<210> 437
<211> 1141
<212> PRT
<213> Homo sapiens

<400> 437
Met Ala Gly Ala Arg Ser Arg Asp Pro Trp Gly Ala Ser Gly Ile
1 5 10 15
Cys Tyr Leu Phe Gly Ser Leu Leu Val Glu Leu Leu Phe Ser Arg
20 25 30
Ala Val Ala Phe Asn Leu Asp Val Met Gly Ala Leu Arg Lys Glu
35 40 45
Gly Glu Pro Gly Ser Leu Phe Gly Phe Ser Val Ala Leu His Arg
50 55 60
Gln Leu Gln Pro Arg Pro Gln Ser Trp Leu Leu Val Gly Ala Pro
65 70 75
Gln Ala Leu Ala Leu Pro Gly Gln Gln Ala Asn Arg Thr Gly Gly

80										85					90				
Leu	Phe	Ala	Cys	Pro	Leu	Ser	Leu	Glu	Glu	Thr	Asp	Cys	Tyr	Arg					
				95					100					105					
Val	Asp	Ile	Asp	Gln	Gly	Ala	Asp	Met	Gln	Lys	Glu	Ser	Lys	Glu					
				110					115					120					
Asn	Gln	Trp	Leu	Gly	Val	Ser	Val	Arg	Ser	Gln	Gly	Pro	Gly	Gly					
				125					130					135					
Lys	Ile	Val	Thr	Cys	Ala	His	Arg	Tyr	Glu	Ala	Arg	Gln	Arg	Val					
				140					145					150					
Asp	Gln	Ile	Leu	Glu	Thr	Arg	Asp	Met	Ile	Gly	Arg	Cys	Phe	Val					
				155					160					165					
Leu	Ser	Gln	Asp	Leu	Ala	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Gly	Glu					
				170					175					180					
Trp	Lys	Phe	Cys	Glu	Gly	Arg	Pro	Gln	Gly	His	Glu	Gln	Phe	Gly					
				185					190					195					
Phe	Cys	Gln	Gln	Gly	Thr	Ala	Ala	Ala	Phe	Ser	Pro	Asp	Ser	His					
				200					205					210					
Tyr	Leu	Leu	Phe	Gly	Ala	Pro	Gly	Thr	Tyr	Asn	Trp	Lys	Gly	Thr					
				215					220					225					
Ala	Arg	Val	Glu	Leu	Cys	Ala	Gln	Gly	Ser	Ala	Asp	Leu	Ala	His					
				230					235					240					
Leu	Asp	Asp	Gly	Pro	Tyr	Glu	Ala	Gly	Gly	Glu	Lys	Glu	Gln	Asp					
				245					250					255					
Pro	Arg	Leu	Ile	Pro	Val	Pro	Ala	Asn	Ser	Tyr	Phe	Gly	Phe	Ser					
				260					265					270					
Ile	Asp	Ser	Gly	Lys	Gly	Leu	Val	Arg	Ala	Glu	Glu	Leu	Ser	Phe					
				275					280					285					
Val	Ala	Gly	Ala	Pro	Arg	Ala	Asn	His	Lys	Gly	Ala	Val	Val	Ile					
				290					295					300					
Leu	Arg	Lys	Asp	Ser	Ala	Ser	Arg	Leu	Val	Pro	Glu	Val	Met	Leu					
				305					310					315					
Ser	Gly	Glu	Arg	Leu	Thr	Ser	Gly	Phe	Gly	Tyr	Ser	Leu	Ala	Val					
				320					325					330					
Ala	Asp	Leu	Asn	Ser	Asp	Gly	Trp	Pro	Asp	Leu	Ile	Val	Gly	Ala					
				335					340					345					
Pro	Tyr	Phe	Phe	Glu	Arg	Gln	Glu	Glu	Leu	Gly	Gly	Ala	Val	Tyr					
				350					355					360					
Val	Tyr	Leu	Asn	Gln	Gly	Gly	His	Trp	Ala	Gly	Ile	Ser	Pro	Leu					
				365					370					375					

Arg	Leu	Cys	Gly	Ser	Pro	Asp	Ser	Met	Phe	Gly	Ile	Ser	Leu	Ala	380	385	390
Val	Leu	Gly	Asp	Leu	Asn	Gln	Asp	Gly	Phe	Pro	Asp	Ile	Ala	Val	395	400	405
Gly	Ala	Pro	Phe	Asp	Gly	Asp	Gly	Lys	Val	Phe	Ile	Tyr	His	Gly	410	415	420
Ser	Ser	Leu	Gly	Val	Val	Ala	Lys	Pro	Ser	Gln	Val	Leu	Glu	Gly	425	430	435
Glu	Ala	Val	Gly	Ile	Lys	Ser	Phe	Gly	Tyr	Ser	Leu	Ser	Gly	Ser	440	445	450
Leu	Asp	Met	Asp	Gly	Asn	Gln	Tyr	Pro	Asp	Leu	Leu	Val	Gly	Ser	455	460	465
Leu	Ala	Asp	Thr	Ala	Val	Leu	Phe	Arg	Ala	Arg	Pro	Ile	Leu	His	470	475	480
Val	Ser	His	Glu	Val	Ser	Ile	Ala	Pro	Arg	Ser	Ile	Asp	Leu	Glu	485	490	495
Gln	Pro	Asn	Cys	Ala	Gly	Gly	His	Ser	Val	Cys	Val	Asp	Leu	Arg	500	505	510
Val	Cys	Phe	Ser	Tyr	Ile	Ala	Val	Pro	Ser	Ser	Tyr	Ser	Pro	Thr	515	520	525
Val	Ala	Leu	Asp	Tyr	Val	Leu	Asp	Ala	Asp	Thr	Asp	Arg	Arg	Leu	530	535	540
Arg	Gly	Gln	Val	Pro	Arg	Val	Thr	Phe	Leu	Ser	Arg	Asn	Leu	Glu	545	550	555
Glu	Pro	Lys	His	Gln	Ala	Ser	Gly	Thr	Val	Trp	Leu	Lys	His	Gln	560	565	570
His	Asp	Arg	Val	Cys	Gly	Asp	Ala	Met	Phe	Gln	Leu	Gln	Glu	Asn	575	580	585
Val	Lys	Asp	Lys	Leu	Arg	Ala	Ile	Val	Val	Thr	Leu	Ser	Tyr	Ser	590	595	600
Leu	Gln	Thr	Pro	Arg	Leu	Arg	Arg	Gln	Ala	Pro	Gly	Gln	Gly	Leu	605	610	615
Pro	Pro	Val	Ala	Pro	Ile	Leu	Asn	Ala	His	Gln	Pro	Ser	Thr	Gln	620	625	630
Arg	Ala	Glu	Ile	His	Phe	Leu	Lys	Gln	Gly	Cys	Gly	Glu	Asp	Lys	635	640	645
Ile	Cys	Gln	Ser	Asn	Leu	Gln	Leu	Val	His	Ala	Arg	Phe	Cys	Thr	650	655	660
Arg	Val	Ser	Asp	Thr	Glu	Phe	Gln	Pro	Leu	Pro	Met	Asp	Val	Asp			

665										670					675				
Gly	Thr	Thr	Ala	Leu	Phe	Ala	Leu	Ser	Gly	Gln	Pro	Val	Ile	Gly					
				680					685					690					
Leu	Glu	Leu	Met	Val	Thr	Asn	Leu	Pro	Ser	Asp	Pro	Ala	Gln	Pro					
				695					700					705					
Gln	Ala	Asp	Gly	Asp	Asp	Ala	His	Glu	Ala	Gln	Leu	Leu	Val	Met					
				710					715					720					
Leu	Pro	Asp	Ser	Leu	His	Tyr	Ser	Gly	Val	Arg	Ala	Leu	Asp	Pro					
				725					730					735					
Ala	Glu	Lys	Pro	Leu	Cys	Leu	Ser	Asn	Glu	Asn	Ala	Ser	His	Val					
				740					745					750					
Glu	Cys	Glu	Leu	Gly	Asn	Pro	Met	Lys	Arg	Gly	Ala	Gln	Val	Thr					
				755					760					765					
Phe	Tyr	Leu	Ile	Leu	Ser	Thr	Ser	Gly	Ile	Ser	Ile	Glu	Thr	Thr					
				770					775					780					
Glu	Leu	Glu	Val	Glu	Leu	Leu	Leu	Ala	Thr	Ile	Ser	Glu	Gln	Glu					
				785					790					795					
Leu	His	Pro	Val	Ser	Ala	Arg	Ala	Arg	Val	Phe	Ile	Glu	Leu	Pro					
				800					805					810					
Leu	Ser	Ile	Ala	Gly	Met	Ala	Ile	Pro	Gln	Gln	Leu	Phe	Phe	Ser					
				815					820					825					
Gly	Val	Val	Arg	Gly	Glu	Arg	Ala	Met	Gln	Ser	Glu	Arg	Asp	Val					
				830					835					840					
Gly	Ser	Lys	Val	Lys	Tyr	Glu	Val	Thr	Val	Ser	Asn	Gln	Gly	Gln					
				845					850					855					
Ser	Leu	Arg	Thr	Leu	Gly	Ser	Ala	Phe	Leu	Asn	Ile	Met	Trp	Pro					
				860					865					870					
His	Glu	Ile	Ala	Asn	Gly	Lys	Trp	Leu	Leu	Tyr	Pro	Met	Gln	Val					
				875					880					885					
Glu	Leu	Glu	Gly	Gly	Gln	Gly	Pro	Gly	Gln	Lys	Gly	Leu	Cys	Ser					
				890					895					900					
Pro	Arg	Pro	Asn	Ile	Leu	His	Leu	Asp	Val	Asp	Ser	Arg	Asp	Arg					
				905					910					915					
Arg	Arg	Arg	Glu	Leu	Glu	Pro	Pro	Glu	Gln	Gln	Glu	Pro	Gly	Glu					
				920					925					930					
Arg	Gln	Glu	Pro	Ser	Met	Ser	Trp	Trp	Pro	Val	Ser	Ser	Ala	Glu					
				935					940					945					
Lys	Lys	Lys	Asn	Ile	Thr	Leu	Asp	Cys	Ala	Arg	Gly	Thr	Ala	Asn					
				950					955					960					

Cys Val Val Phe Ser Cys Pro Leu Tyr Ser Phe Asp Arg Ala Ala
965 970 975

Val Leu His Val Trp Gly Arg Leu Trp Asn Ser Thr Phe Leu Glu
980 985 990

Glu Tyr Ser Ala Val Lys Ser Leu Glu Val Ile Val Arg Ala Asn
995 1000 1005

Ile Thr Val Lys Ser Ser Ile Lys Asn Leu Met Leu Arg Asp Ala
1010 1015 1020

Ser Thr Val Ile Pro Val Met Val Tyr Leu Asp Pro Met Ala Val
1025 1030 1035

Val Ala Glu Gly Val Pro Trp Trp Val Ile Leu Leu Ala Val Leu
1040 1045 1050

Ala Gly Leu Leu Val Leu Ala Leu Leu Val Leu Leu Leu Trp Lys
1055 1060 1065

Met Gly Phe Phe Lys Arg Ala Lys His Pro Glu Ala Thr Val Pro
1070 1075 1080

Gln Tyr His Ala Val Lys Ile Pro Arg Glu Asp Arg Gln Gln Phe
1085 1090 1095

Lys Glu Glu Lys Thr Gly Thr Ile Leu Arg Asn Asn Trp Gly Ser
1100 1105 1110

Pro Arg Arg Glu Gly Pro Asp Ala His Pro Ile Leu Ala Ala Asp
1115 1120 1125

Gly His Pro Glu Leu Gly Pro Asp Gly His Pro Gly Pro Gly Thr
1130 1135 1140

Ala

<210> 438
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<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 438
ggctgacacc gcagtgtctt tcag 24

<210> 439
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 439
gctgctgggg actgcaatgt agct 24

<210> 440

<211> 46

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 440

catcctccat gtctcccatg aggtctctat tgctccacga agcatc 46

<210> 441

<211> 1964

<212> DNA

<213> Homo sapiens

<400> 441

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ggagctgcga gcacagtgtt ggctcacaac aagatgctca aggtgtcagc 150
cgtactgtgt gtgtgtgcag ccgcttggtg cagtcagtct ctcgcagctg 200
ccgcggcggg ggctgcagcc gggggggcgg cggacggcgg taattttctg 250
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acagtggaaac aaattccgag acgaagtaga ggatgattat ttccgcactt 350
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tgcttaaaga tgaaatgtag tcgccataaa gtatgcattg ctcaagattc 450
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gtttaacaga cttgatacaa actatgacct gctattggac cagtcagagc 950

				50						55					60	
Phe	Arg	Asp	Glu	Val	Glu	Asp	Asp	Tyr	Phe	Arg	Thr	Trp	Ser	Pro		
				65					70					75		
Gly	Lys	Pro	Phe	Asp	Gln	Ala	Leu	Asp	Pro	Ala	Lys	Asp	Pro	Cys		
				80					85					90		
Leu	Lys	Met	Lys	Cys	Ser	Arg	His	Lys	Val	Cys	Ile	Ala	Gln	Asp		
				95					100					105		
Ser	Gln	Thr	Ala	Val	Cys	Ile	Ser	His	Arg	Arg	Leu	Thr	His	Arg		
				110					115					120		
Met	Lys	Glu	Ala	Gly	Val	Asp	His	Arg	Gln	Trp	Arg	Gly	Pro	Ile		
				125					130					135		
Leu	Ser	Thr	Cys	Lys	Gln	Cys	Pro	Val	Val	Tyr	Pro	Ser	Pro	Val		
				140					145					150		
Cys	Gly	Ser	Asp	Gly	His	Thr	Tyr	Ser	Phe	Gln	Cys	Lys	Leu	Glu		
				155					160					165		
Tyr	Gln	Ala	Cys	Val	Leu	Gly	Lys	Gln	Ile	Ser	Val	Lys	Cys	Glu		
				170					175					180		
Gly	His	Cys	Pro	Cys	Pro	Ser	Asp	Lys	Pro	Thr	Ser	Thr	Ser	Arg		
				185					190					195		
Asn	Val	Lys	Arg	Ala	Cys	Ser	Asp	Leu	Glu	Phe	Arg	Glu	Val	Ala		
				200					205					210		
Asn	Arg	Leu	Arg	Asp	Trp	Phe	Lys	Ala	Leu	His	Glu	Ser	Gly	Ser		
				215					220					225		
Gln	Asn	Lys	Lys	Thr	Lys	Thr	Leu	Leu	Arg	Pro	Glu	Arg	Ser	Arg		
				230					235					240		
Phe	Asp	Thr	Ser	Ile	Leu	Pro	Ile	Cys	Lys	Asp	Ser	Leu	Gly	Trp		
				245					250					255		
Met	Phe	Asn	Arg	Leu	Asp	Thr	Asn	Tyr	Asp	Leu	Leu	Leu	Asp	Gln		
				260					265					270		
Ser	Glu	Leu	Arg	Ser	Ile	Tyr	Leu	Asp	Lys	Asn	Glu	Gln	Cys	Thr		
				275					280					285		
Lys	Ala	Phe	Phe	Asn	Ser	Cys	Asp	Thr	Tyr	Lys	Asp	Ser	Leu	Ile		
				290					295					300		
Ser	Asn	Asn	Glu	Trp	Cys	Tyr	Cys	Phe	Gln	Arg	Gln	Gln	Asp	Pro		
				305					310					315		
Pro	Cys	Gln	Thr	Glu	Leu	Ser	Asn	Ile	Gln	Lys	Arg	Gln	Gly	Val		
				320					325					330		
Lys	Lys	Leu	Leu	Gly	Gln	Tyr	Ile	Pro	Leu	Cys	Asp	Glu	Asp	Gly		
				335					340					345		

Tyr	Tyr	Lys	Pro	Thr	Gln	Cys	His	Gly	Ser	Val	Gly	Gln	Cys	Trp
				350					355					360
Cys	Val	Asp	Arg	Tyr	Gly	Asn	Glu	Val	Met	Gly	Ser	Arg	Ile	Asn
				365					370					375
Gly	Val	Ala	Asp	Cys	Ala	Ile	Asp	Phe	Glu	Ile	Ser	Gly	Asp	Phe
				380					385					390
Ala	Ser	Gly	Asp	Phe	His	Glu	Trp	Thr	Asp	Asp	Glu	Asp	Asp	Glu
				395					400					405
Asp	Asp	Ile	Met	Asn	Asp	Glu	Asp	Glu	Ile	Glu	Asp	Asp	Asp	Glu
				410					415					420
Asp	Glu	Gly	Asp	Asp	Asp	Asp	Gly	Gly	Asp	Asp	His	Asp	Val	Tyr
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Ile

<210> 443

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 443

cagcaatatt cagaagcggc aaggg 25

<210> 444

<211> 28

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 444

catcatggtc atcaccacca tcatcatc 28

<210> 445

<211> 48

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 445

ggttactaca agccaacaca atgtcatggc agtggtggac agtgctgg 48

<210> 446

<211> 3617

<212> DNA

<213> Homo sapiens

<400> 446

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cagggatggg cgacaagatc tggctgccct tccccgtgct cttcttgccc 150
gctctgcctc cgggtgctgt gcttggggcg gccggcttca caccttccct 200
cgatagcgac ttcaccttta cccttcccgc cggccagaag gagtgtttct 250
accagcccat gccoctgaag gcctcgctgg agatcgagta ccaagtttta 300
gatggagcag gattagatat tgatttccat cttgcctctc cagaaggcaa 350
aaccttagtt tttgaacaaa gaaaatcaga tggagttcac actgtagaga 400
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tggatatgaa actggaagac atcctggaat ccatcaacag catcaagtcc 600
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 aaattatcaa aggaaaa 3617

<210> 447
 <211> 229
 <212> PRT
 <213> Homo sapiens

<400> 447
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 20 25 30
 Ser Leu Asp Ser Asp Phe Thr Phe Thr Leu Pro Ala Gly Gln Lys
 35 40 45
 Glu Cys Phe Tyr Gln Pro Met Pro Leu Lys Ala Ser Leu Glu Ile
 50 55 60
 Glu Tyr Gln Val Leu Asp Gly Ala Gly Leu Asp Ile Asp Phe His
 65 70 75
 Leu Ala Ser Pro Glu Gly Lys Thr Leu Val Phe Glu Gln Arg Lys
 80 85 90
 Ser Asp Gly Val His Thr Val Glu Thr Glu Val Gly Asp Tyr Met
 95 100 105
 Phe Cys Phe Asp Asn Thr Phe Ser Thr Ile Ser Glu Lys Val Ile

	110		115		120
Phe Phe Glu Leu	Ile Leu Asp Asn Met	Gly Glu Gln Ala Gln Glu			
	125	130			135
Gln Glu Asp Trp	Lys Lys Tyr Ile Thr	Gly Thr Asp Ile Leu Asp			
	140	145			150
Met Lys Leu Glu	Asp Ile Leu Glu Ser	Ile Asn Ser Ile Lys Ser			
	155	160			165
Arg Leu Ser Lys	Ser Gly His Ile Gln	Ile Leu Leu Arg Ala Phe			
	170	175			180
Glu Ala Arg Asp	Arg Asn Ile Gln Glu	Ser Asn Phe Asp Arg Val			
	185	190			195
Asn Phe Trp Ser	Met Val Asn Leu Val	Val Met Val Val Val Ser			
	200	205			210
Ala Ile Gln Val	Tyr Met Leu Lys Ser	Leu Phe Glu Asp Lys Arg			
	215	220			225
Lys Ser Arg Thr					

<210> 448
 <211> 23
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 448
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<210> 449
 <211> 23
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 449
 gtcttccagt ttcatatcca ata 23

<210> 450
 <211> 43
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 450
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<210> 451
 <211> 859
 <212> DNA
 <213> Homo sapiens

<400> 451
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 gccctgccca gtgtgtcctg gatgctgctt tctgcctca ttctcctgtg 150
 tcaggttcaa ggtgaagaaa ccagaagga actgccctct ccacggatca 200
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 aaaaaaaaaa 859

<210> 452
 <211> 175
 <212> PRT
 <213> Homo sapiens

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 20 25 30
 Lys Glu Leu Pro Ser Pro Arg Ile Ser Cys Pro Lys Gly Ser Lys
 35 40 45
 Ala Tyr Gly Ser Pro Cys Tyr Ala Leu Phe Leu Ser Pro Lys Ser

50	55	60
Trp Met Asp Ala Asp Leu Ala Cys Gln Lys Arg Pro Ser Gly Lys		
65	70	75
Leu Val Ser Val Leu Ser Gly Ala Glu Gly Ser Phe Val Ser Ser		
80	85	90
Leu Val Arg Ser Ile Ser Asn Ser Tyr Ser Tyr Ile Trp Ile Gly		
95	100	105
Leu His Asp Pro Thr Gln Gly Ser Glu Pro Asp Gly Asp Gly Trp		
110	115	120
Glu Trp Ser Ser Thr Asp Val Met Asn Tyr Phe Ala Trp Glu Lys		
125	130	135
Asn Pro Ser Thr Ile Leu Asn Pro Gly His Cys Gly Ser Leu Ser		
140	145	150
Arg Ser Thr Gly Phe Leu Lys Trp Lys Asp Tyr Asn Cys Asp Ala		
155	160	165
Lys Leu Pro Tyr Val Cys Lys Phe Lys Asp		
170	175	

<210> 453
 <211> 550
 <212> DNA
 <213> Homo sapiens

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 ggcgctcctg gcgctggtgc tggctgcctg cggagagctg gcgccggccc 150
 tgcgctgcta cgtctgtccg gagccacag gagtgtcgga ctgtgtcacc 200
 atcgccacct gcaccaccaa cgaaacctg tgcaagacca cactctactc 250
 ccgggagata gtgtaccct tccaggggga ctccacggtg accaagtcct 300
 gtgccagcaa gtgtaagccc tcggatgtgg atggcatcgg ccagaccctg 350
 cccgtgtcct gctgcaatac tgagctgtgc aatgtagacg gggcgccccgc 400
 tctgaacagc ctccactgcg gggccctcac gctcctcca ctcttgagcc 450
 tccgactgta gagtccccgc ccaccccat ggccctatgc ggcccagccc 500
 cgaatgcctt gaagaagtgc cccctgcacc aggaaaaaaa aaaaaaaaaa 550

<210> 454
 <211> 125
 <212> PRT
 <213> Homo sapiens

<400> 454

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			20						25					30
Pro	Thr	Gly	Val	Ser	Asp	Cys	Val	Thr	Ile	Ala	Thr	Cys	Thr	Thr
				35					40					45
Asn	Glu	Thr	Met	Cys	Lys	Thr	Thr	Leu	Tyr	Ser	Arg	Glu	Ile	Val
				50					55					60
Tyr	Pro	Phe	Gln	Gly	Asp	Ser	Thr	Val	Thr	Lys	Ser	Cys	Ala	Ser
				65					70					75
Lys	Cys	Lys	Pro	Ser	Asp	Val	Asp	Gly	Ile	Gly	Gln	Thr	Leu	Pro
				80					85					90
Val	Ser	Cys	Cys	Asn	Thr	Glu	Leu	Cys	Asn	Val	Asp	Gly	Ala	Pro
				95					100					105
Ala	Leu	Asn	Ser	Leu	His	Cys	Gly	Ala	Leu	Thr	Leu	Leu	Pro	Leu
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				125										

<210> 455

<211> 1518

<212> DNA

<213> Homo sapiens

<400> 455

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Glu	Glu	Thr	Ile	Thr	Glu	Ser	Phe	Gly	Asn	Asp	His	Ser	Thr	Leu	155	160	165
Asp	Gly	Tyr	Ser	Arg	Arg	Thr	Thr	Leu	Ser	Ser	Lys	Met	Tyr	His	170	175	180
Thr	Lys	Gly	Gln	Glu	Gly	Ser	Val	Cys	Leu	Arg	Ser	Ser	Asp	Cys	185	190	195
Ala	Ser	Gly	Leu	Cys	Cys	Ala	Arg	His	Phe	Trp	Ser	Lys	Ile	Cys	200	205	210
Lys	Pro	Val	Leu	Lys	Glu	Gly	Gln	Val	Cys	Thr	Lys	His	Arg	Arg	215	220	225
Lys	Gly	Ser	His	Gly	Leu	Glu	Ile	Phe	Gln	Arg	Cys	Tyr	Cys	Gly	230	235	240
Glu	Gly	Leu	Ser	Cys	Arg	Ile	Gln	Lys	Asp	His	His	Gln	Ala	Ser	245	250	255
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<211> 638

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

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<223> unknown base

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 <213> Homo sapiens

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 Ala Ser Ser Arg Glu Ile Arg Gln Ala Phe Lys Lys Leu Ala Leu
 50 55 60
 Lys Leu His Pro Asp Lys Asn Pro Asn Asn Pro Asn Ala His Gly
 65 70 75
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 80 85 90
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 Asp Asn Gln Gly Gly Gln Tyr Glu Ser Trp Asn Tyr Tyr Arg Tyr
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 Asp Phe Gly Ile Tyr Asp Asp Asp Pro Glu Ile Ile Thr Leu Glu
 125 130 135
 Arg Arg Glu Phe Asp Ala Ala Val Asn Ser Gly Glu Leu Trp Phe
 140 145 150
 Val Asn Phe Tyr Ser Pro Gly Cys Ser His Cys His Asp Leu Ala
 155 160 165
 Pro Thr Trp Arg Asp Phe Ala Lys Glu Val Asp Gly Leu Leu Arg
 170 175 180
 Ile Gly Ala Val Asn Cys Gly Asp Asp Arg Met Leu Cys Arg Met
 185 190 195
 Lys Gly Val Asn Ser Tyr Pro Ser Leu Phe Ile Phe Arg Ser Gly

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	230	235	240		
Trp Thr Gly Asn	Phe Val Asn Ser Ile	Gln Thr Ala Phe Ala	Ala		
	245	250	255		
Gly Ile Gly Trp	Leu Ile Thr Phe Cys	Ser Lys Gly Gly Asp	Cys		
	260	265	270		
Leu Thr Ser Gln	Thr Arg Leu Arg Leu	Ser Gly Met Leu Phe	Leu		
	275	280	285		
Asn Ser Leu Asp	Ala Lys Glu Ile Tyr	Leu Glu Val Ile His	Asn		
	290	295	300		
Leu Pro Asp Phe	Glu Leu Leu Ser Ala	Asn Thr Leu Glu Asp	Arg		
	305	310	315		
Leu Ala His His	Arg Trp Leu Leu Phe	Phe His Phe Gly Lys	Asn		
	320	325	330		
Glu Asn Ser Asn	Asp Pro Glu Leu Lys	Lys Leu Lys Thr Leu	Leu		
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Lys Asn Asp His	Ile Gln Val Gly Arg	Phe Asp Cys Ser Ser	Ala		
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Asp Lys Glu Pro	Trp Leu Val Asp Phe	Phe Ala Pro Trp Cys	Pro		
	425	430	435		
Pro Cys Arg Ala	Leu Leu Pro Glu Leu	Arg Arg Ala Ser Asn	Leu		
	440	445	450		
Leu Tyr Gly Gln	Leu Lys Phe Gly Thr	Leu Asp Cys Thr Val	His		
	455	460	465		
Glu Gly Leu Cys	Asn Met Tyr Asn Ile	Gln Ala Tyr Pro Thr	Thr		
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Val Val Phe Asn	Gln Ser Asn Ile His	Glu Tyr Glu Gly His	His		
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Trp	Cys	His	Pro	Cys	Gln	Val	Leu	Met	Pro	Glu	Trp	Lys	Arg	Met	
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Ala	Arg	Thr	Leu	Thr	Gly	Leu	Ile	Asn	Val	Gly	Ser	Ile	Asp	Cys	
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Gln	Gln	Tyr	His	Ser	Phe	Cys	Ala	Gln	Glu	Asn	Val	Gln	Arg	Tyr	
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Pro	Glu	Ile	Arg	Phe	Phe	Pro	Pro	Lys	Ser	Asn	Lys	Ala	Tyr	Gln	
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Tyr	His	Ser	Tyr	Asn	Gly	Trp	Asn	Arg	Asp	Ala	Tyr	Ser	Leu	Arg	
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Lys	Ala	Gly	Lys	Val	Asp	Cys	Gln	Ala	Tyr	Ala	Gln	Thr	Cys	Gln	
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Lys	Ala	Gly	Ile	Arg	Ala	Tyr	Pro	Thr	Val	Lys	Phe	Tyr	Phe	Tyr	
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<223> Synthetic oligonucleotide probe

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<212> DNA

<213> Artificial Sequence

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<223> Synthetic oligonucleotide probe

<400> 461

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<210> 462

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<213> Artificial Sequence

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<223> Synthetic oligonucleotide probe

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<212> DNA

<213> Homo sapiens

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 <212> PRT
 <213> Homo sapiens

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Ser	Ile	Leu	Val	Leu	Trp	Asp	Ile	Asn	Lys	Arg	Gly	Val	Glu	Glu		65	70	75
Thr	Ala	Ala	Glu	Cys	Arg	Lys	Leu	Gly	Val	Thr	Ala	His	Ala	Tyr		80	85	90
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Glu	Ile	Thr	Lys	Thr	Phe	Glu	Val	Asn	Ile	Leu	Gly	His	Phe	Trp		140	145	150
Ile	Thr	Lys	Ala	Leu	Leu	Pro	Ser	Met	Met	Glu	Arg	Asn	His	Gly		155	160	165
His	Ile	Val	Thr	Val	Ala	Ser	Val	Cys	Gly	His	Glu	Gly	Ile	Pro		170	175	180
Tyr	Leu	Ile	Pro	Tyr	Cys	Ser	Ser	Lys	Phe	Ala	Ala	Val	Gly	Phe		185	190	195
His	Arg	Gly	Leu	Thr	Ser	Glu	Leu	Gln	Ala	Leu	Gly	Lys	Thr	Gly		200	205	210
Ile	Lys	Thr	Ser	Cys	Leu	Cys	Pro	Val	Phe	Val	Asn	Thr	Gly	Phe		215	220	225
Thr	Lys	Asn	Pro	Ser	Thr	Arg	Leu	Trp	Pro	Val	Leu	Glu	Thr	Asp		230	235	240
Glu	Val	Val	Arg	Ser	Leu	Ile	Asp	Gly	Ile	Leu	Thr	Asn	Lys	Lys		245	250	255
Met	Ile	Phe	Val	Pro	Ser	Tyr	Ile	Asn	Ile	Phe	Leu	Arg	Leu	Gln		260	265	270
Lys	Phe	Leu	Pro	Glu	Arg	Ala	Ser	Ala	Ile	Leu	Asn	Arg	Met	Gln		275	280	285
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<211> 1547

<212> DNA

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Phe	Leu	Phe	Val	Arg	Asp	Pro	Phe	Val	Arg	Leu	Ile	Ser	Ala	Phe	
				245					250					255	
Arg	Ser	Lys	Phe	Glu	Leu	Glu	Asn	Glu	Glu	Phe	Tyr	Arg	Lys	Phe	
				260					265					270	
Ala	Val	Pro	Met	Leu	Arg	Leu	Tyr	Ala	Asn	His	Thr	Ser	Leu	Pro	
				275					280					285	
Ala	Ser	Ala	Arg	Glu	Ala	Phe	Arg	Ala	Gly	Leu	Lys	Val	Ser	Phe	
				290					295					300	
Ala	Asn	Phe	Ile	Gln	Tyr	Leu	Leu	Asp	Pro	His	Thr	Glu	Lys	Leu	
				305					310					315	
Ala	Pro	Phe	Asn	Glu	His	Trp	Arg	Gln	Val	Tyr	Arg	Leu	Cys	His	
				320					325					330	
Pro	Cys	Gln	Ile	Asp	Tyr	Asp	Phe	Val	Gly	Lys	Leu	Glu	Thr	Leu	
				335					340					345	
Asp	Glu	Asp	Ala	Ala	Gln	Leu	Leu	Gln	Leu	Leu	Gln	Val	Asp	Arg	
				350					355					360	
Gln	Leu	Arg	Phe	Pro	Pro	Ser	Tyr	Arg	Asn	Arg	Thr	Ala	Ser	Ser	
				365					370					375	
Trp	Glu	Glu	Asp	Trp	Phe	Ala	Lys	Ile	Pro	Leu	Ala	Trp	Arg	Gln	
				380					385					390	
Gln	Leu	Tyr	Lys	Leu	Tyr	Glu	Ala	Asp	Phe	Val	Leu	Phe	Gly	Tyr	
				395					400					405	
Pro	Lys	Pro	Glu	Asn	Leu	Leu	Arg	Asp							
				410											

<210> 467
 <211> 1071
 <212> DNA
 <213> Homo sapiens

<400> 467
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 ctttggaggt gaaagaggcc cagagtagag agagagagag accgacgtac 100
 acgggatggc tacgggaacg cgctatgccg ggaaggtggt ggtcgtgacc 150
 gggggcgggc gcggcacg agctgggatc gtgcgcgcct togtgaacag 200
 cggggcccca gtggttatct gcgacaagga tgagtctggg ggccgggccc 250
 tggagcagga gctccctgga gctgtcttta tcctctgtga tgtgactcag 300
 gaagatgatg tgaagaccct ggtttctgag accatccgcc gatttgccg 350
 cctggattgt gttgtcaaca acgctggcca ccacccaccc ccacagaggc 400

ctgaggagac ctctgccag ggattccgcc agctgctgga gctgaaccta 450
ctggggacgt acaccttgac caagctcgcc ctcccctacc tgcggaagag 500
tcaagggaaat gtcacaaaca tctccagcct ggtgggggca atcgccagg 550
cccaggcagt tccctatgtg gccaccaagg gggcagtaac agccatgacc 600
aaagctttgg ccctggatga aagtccatat ggtgtccgag tcaactgtat 650
ctccccagga aacatctgga ccccgctgtg ggaggagctg gcagccttaa 700
tgccagaccc tagggccaca atccgagagg gcatgctggc ccagccactg 750
ggccgcatgg gccagcccg ctaggtcggg gctgcggcag tgttcctggc 800
ctccgaagcc aacttctgca cgggcattga actgctgtg acggggggtg 850
cagagctggg gtacgggtgc aaggccagtc ggagcacccc cgtggacgcc 900
cccgatatcc cttcctgatt tctctcatth ctacttgggg ccccttcct 950
aggactctcc caccctaaac tccaacctgt atcagatgca gcccccaagc 1000
ccttagactc taagccagc tagcaagggtg ccgggtcacc ctgcagggtc 1050
ccataaaaac gatttgcagc c 1071

<210> 468
<211> 270
<212> PRT
<213> Homo sapiens

<400> 468
Met Ala Thr Gly Thr Arg Tyr Ala Gly Lys Val Val Val Val Thr
1 5 10 15
Gly Gly Gly Arg Gly Ile Gly Ala Gly Ile Val Arg Ala Phe Val
20 25 30
Asn Ser Gly Ala Arg Val Val Ile Cys Asp Lys Asp Glu Ser Gly
35 40 45
Gly Arg Ala Leu Glu Gln Glu Leu Pro Gly Ala Val Phe Ile Leu
50 55 60
Cys Asp Val Thr Gln Glu Asp Asp Val Lys Thr Leu Val Ser Glu
65 70 75
Thr Ile Arg Arg Phe Gly Arg Leu Asp Cys Val Val Asn Asn Ala
80 85 90
Gly His His Pro Pro Pro Gln Arg Pro Glu Glu Thr Ser Ala Gln
95 100 105
Gly Phe Arg Gln Leu Leu Glu Leu Asn Leu Leu Gly Thr Tyr Thr
110 115 120

Leu Thr Lys Leu	Ala Leu Pro Tyr Leu	Arg Lys Ser Gln Gly Asn	
	125	130	135
Val Ile Asn Ile	Ser Ser Leu Val Gly	Ala Ile Gly Gln Ala Gln	
	140	145	150
Ala Val Pro Tyr	Val Ala Thr Lys Gly	Ala Val Thr Ala Met Thr	
	155	160	165
Lys Ala Leu Ala	Leu Asp Glu Ser Pro	Tyr Gly Val Arg Val Asn	
	170	175	180
Cys Ile Ser Pro	Gly Asn Ile Trp Thr	Pro Leu Trp Glu Glu Leu	
	185	190	195
Ala Ala Leu Met	Pro Asp Pro Arg Ala	Thr Ile Arg Glu Gly Met	
	200	205	210
Leu Ala Gln Pro	Leu Gly Arg Met Gly	Gln Pro Ala Glu Val Gly	
	215	220	225
Ala Ala Ala Val	Phe Leu Ala Ser Glu	Ala Asn Phe Cys Thr Gly	
	230	235	240
Ile Glu Leu Leu	Val Thr Gly Gly Ala	Glu Leu Gly Tyr Gly Cys	
	245	250	255
Lys Ala Ser Arg	Ser Thr Pro Val Asp	Ala Pro Asp Ile Pro Ser	
	260	265	270

<210> 469
 <211> 687
 <212> DNA
 <213> Homo sapiens

<400> 469
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 cctcacaacc tgctgtttct tcttaccatt tccatcttcc tggggctggg 100
 ccagcccagg agccccaaaa gcaagaggaa ggggcaaggg cggcctgggc 150
 ccctggcccc tggccctcac caggtgccac tggacctggt gtcacggatg 200
 aaaccgtatg cccgcatgga ggagtatgag aggaacatcg aggagatggt 250
 ggcccagctg aggaacagct cagagctggc ccagagaaaag tgtgaggtca 300
 acttgcagct gtggatgtcc aacaagagga gcctgtctcc ctggggctac 350
 agcatcaacc acgaccccag ccgtatcccc gtggacctgc cggaggcacg 400
 gtgcctgtgt ctgggctgtg tgaaccctt caccatgcag gaggaccgca 450
 gcatggtgag cgtgccggtg ttcagccagg ttcctgtgcg ccgccgctc 500
 tgcccgcac cgcgccgcac agggccttgc cgccagcgcg cagtcatgga 550

gaccatcgct gtgggctgca cctgcatott ctgaatcacc tggcccagaa 600
gccaggccag cagcccagaga ccatactcct tgcacctttg tgccaagaaa 650
ggcctatgaa aagtaaacac tgacttttga aagcaag 687

<210> 470
<211> 180
<212> PRT
<213> Homo sapiens

<400> 470
Met Asp Trp Pro His Asn Leu Leu Phe Leu Leu Thr Ile Ser Ile
1 5 10 15
Phe Leu Gly Leu Gly Gln Pro Arg Ser Pro Lys Ser Lys Arg Lys
20 25 30
Gly Gln Gly Arg Pro Gly Pro Leu Ala Pro Gly Pro His Gln Val
35 40 45
Pro Leu Asp Leu Val Ser Arg Met Lys Pro Tyr Ala Arg Met Glu
50 55 60
Glu Tyr Glu Arg Asn Ile Glu Glu Met Val Ala Gln Leu Arg Asn
65 70 75
Ser Ser Glu Leu Ala Gln Arg Lys Cys Glu Val Asn Leu Gln Leu
80 85 90
Trp Met Ser Asn Lys Arg Ser Leu Ser Pro Trp Gly Tyr Ser Ile
95 100 105
Asn His Asp Pro Ser Arg Ile Pro Val Asp Leu Pro Glu Ala Arg
110 115 120
Cys Leu Cys Leu Gly Cys Val Asn Pro Phe Thr Met Gln Glu Asp
125 130 135
Arg Ser Met Val Ser Val Pro Val Phe Ser Gln Val Pro Val Arg
140 145 150
Arg Arg Leu Cys Pro Pro Pro Pro Arg Thr Gly Pro Cys Arg Gln
155 160 165
Arg Ala Val Met Glu Thr Ile Ala Val Gly Cys Thr Cys Ile Phe
170 175 180

<210> 471
<211> 2368
<212> DNA
<213> Homo sapiens

<400> 471
gcgcccgcag gcgtaggcgg ggtggccctt gcgtotcccg cttccttgaa 50
aaacccggcg ggcgagcgag gctgcgggcc ggccgctgcc cttccccaca 100

ctccccgccg agaagcctcg ctcggcgccc aacatggcgg gtgggcgctg 150
 cggcccgag ctaacgggcg tcctggccgc ctggatcgcg gctgtggcgg 200
 cgacggcagg ccccgaggag gccgcgctgc cgccggagca gagccgggtc 250
 cagcccatga ccgcctccaa ctggacgctg gtgatggagg gcgagtggat 300
 gctgaaatct tacgccccat ggtgtccatc ctgccagcag actgattcag 350
 aatgggaggc ttttgcaaag aatggtgaaa tacttcagat cagtgtgggg 400
 aaggtagatg tcattcaaga accaggtttg agtggccgct tctttgtcac 450
 cactctccca gcattttttc atgcaaagga tgggatattc cgccgttatt 500
 gtggcccagg aatcttcgaa gacctgcaga attatatctt agagaagaaa 550
 tggcaatcag tcgagcctct gactggctgg aaatccccag cttctctaac 600
 gatgtctgga atggctggtc ttttagcat ctctggcaag atatggcatc 650
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 gtgtttttcg tcatagccac cttggttttt ggcttttta tgggtctggt 750
 cttggtggta atatcagaat gtttctatgt gccacttcca aggcatttat 800
 ctgagcgctt tgagcagaat cggagatcag aggaggctca tagagctgaa 850
 cagttgcagg atgcggagga ggaaaaagat gattcaaag aagaagaaa 900
 caaagacagc cttgtagatg atgaagaaga gaaagaagat cttggcgatg 950
 aggatgaagc agaggaagaa gaggaggagg acaacttggc tgctggtgtg 1000
 gatgaggaga gaagtgggc caatgatcag gggccccag gagaggacgg 1050
 tgtgaccgag gaggaagtag agcctgagga ggctgaagaa ggcattctctg 1100
 agcaaccctg cccagctgac acagagggtg tggaagactc cttgaggcag 1150
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 ctctctagtc atttggctc atggcagtaa gcctcatgta tactaaggag 1350
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 ttacatgaac tgtgtttgtt cattctgacc taaggggttt agataatcag 1900
 taaccataac ccctgaagct gtgactgcc aacatctcaa atgaaatgtt 1950
 gtggccatca gagactcaaa aggaagtaag gatttttaca gacagattaa 2000
 aaaaaaattg ttttgtccaa aatatagttg ttgttgattt ttttttaagt 2050
 tttctaagca atatttttca agccagaagt cctctaagtc ttgccagtac 2100
 aaggtagtct tgtgaagaaa agttgaatac tgttttgttt tcatctcaag 2150
 gggttccctg ggtcttgaac tactttaata ataactaaaa aaccacttct 2200
 gatttttctt cagtgatgtg cttttgggtg aagaattaat gaactccagt 2250
 acctgaaagt gaaagatttg attttgttcc catcttctgt aatottocaa 2300
 agaattatat ctttgtaaatt ctctcaatac tcaatctact gtaagtaccc 2350
 agggaggcta atttcttt 2368

<210> 472
 <211> 349
 <212> PRT
 <213> Homo sapiens

<400> 472
 Met Ala Gly Gly Arg Cys Gly Pro Gln Leu Thr Ala Leu Leu Ala
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 Ala Trp Ile Ala Ala Val Ala Ala Thr Ala Gly Pro Glu Glu Ala
 20 25 30
 Ala Leu Pro Pro Glu Gln Ser Arg Val Gln Pro Met Thr Ala Ser
 35 40 45
 Asn Trp Thr Leu Val Met Glu Gly Glu Trp Met Leu Lys Phe Tyr
 50 55 60
 Ala Pro Trp Cys Pro Ser Cys Gln Gln Thr Asp Ser Glu Trp Glu
 65 70 75
 Ala Phe Ala Lys Asn Gly Glu Ile Leu Gln Ile Ser Val Gly Lys
 80 85 90

Val	Asp	Val	Ile	Gln	Glu	Pro	Gly	Leu	Ser	Gly	Arg	Phe	Phe	Val
				95					100					105
Thr	Thr	Leu	Pro	Ala	Phe	Phe	His	Ala	Lys	Asp	Gly	Ile	Phe	Arg
				110					115					120
Arg	Tyr	Arg	Gly	Pro	Gly	Ile	Phe	Glu	Asp	Leu	Gln	Asn	Tyr	Ile
				125					130					135
Leu	Glu	Lys	Lys	Trp	Gln	Ser	Val	Glu	Pro	Leu	Thr	Gly	Trp	Lys
				140					145					150
Ser	Pro	Ala	Ser	Leu	Thr	Met	Ser	Gly	Met	Ala	Gly	Leu	Phe	Ser
				155					160					165
Ile	Ser	Gly	Lys	Ile	Trp	His	Leu	His	Asn	Tyr	Phe	Thr	Val	Thr
				170					175					180
Leu	Gly	Ile	Pro	Ala	Trp	Cys	Ser	Tyr	Val	Phe	Phe	Val	Ile	Ala
				185					190					195
Thr	Leu	Val	Phe	Gly	Leu	Phe	Met	Gly	Leu	Val	Leu	Val	Val	Ile
				200					205					210
Ser	Glu	Cys	Phe	Tyr	Val	Pro	Leu	Pro	Arg	His	Leu	Ser	Glu	Arg
				215					220					225
Ser	Glu	Gln	Asn	Arg	Arg	Ser	Glu	Glu	Ala	His	Arg	Ala	Glu	Gln
				230					235					240
Leu	Gln	Asp	Ala	Glu	Glu	Glu	Lys	Asp	Asp	Ser	Asn	Glu	Glu	Glu
				245					250					255
Asn	Lys	Asp	Ser	Leu	Val	Asp	Asp	Glu	Glu	Glu	Lys	Glu	Asp	Leu
				260					265					270
Gly	Asp	Glu	Asp	Glu	Ala	Glu	Glu	Glu	Glu	Glu	Glu	Asp	Asn	Leu
				275					280					285
Ala	Ala	Gly	Val	Asp	Glu	Glu	Arg	Ser	Glu	Ala	Asn	Asp	Gln	Gly
				290					295					300
Pro	Pro	Gly	Glu	Asp	Gly	Val	Thr	Arg	Glu	Glu	Val	Glu	Pro	Glu
				305					310					315
Glu	Ala	Glu	Glu	Gly	Ile	Ser	Glu	Gln	Pro	Cys	Pro	Ala	Asp	Thr
				320					325					330
Glu	Val	Val	Glu	Asp	Ser	Leu	Arg	Gln	Arg	Lys	Ser	Gln	His	Ala
				335					340					345

Asp Lys Gly Leu

<210> 473

<211> 24

<212> DNA

<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 473
gtccagccca tgaccgcctc caac 24

<210> 474
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 474
ctctoctcat ccacaccagc agcc 24

<210> 475
<211> 44
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 475
gtggatgctg aaattttacg ccccatgggtg tccatcctgc cagc 44

<210> 476
<211> 2478
<212> DNA
<213> Homo sapiens

<400> 476
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gccacatga ttgactcag agattctctt ttgtccacag acagtcactc 100
caggggcaga aagaaaagag ctcccaaag ctatatctat tcaggggctc 150
tcaagaacaa tggaatatca tcctgattta gaaaatttgg atgaagatgg 200
atatactcaa ttacacttcg actctcaaag caataccagg atagctgttg 250
tttcagagaa aggatogtgt gctgcatctc ctccctggcg cctcattgct 300
gtaatttttg gaatcctatg cttggtaata ctggtgatag ctgtggtcct 350
gggtaccatg ggggttcttt ccagcccttg tcctccta atggattatat 400
atgagaagag ctgttatcta ttcagcatgt cactaaattc ctgggatgga 450
agtaaaagac aatgctggca actgggctct aatctcctaa agatagacag 500
ctcaaagtaa ttgggattta tagtaaaaca agtgtcttcc caacctgata 550
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 agataaatgc agaaaatggt tagagagctt ggccaactgt aatcttaacc 900
 aagaaattga agggagaggc tgtgatttct gtatttgtcg acctacaggt 950
 aggctagtat ttttttcta gttagtagat ccctagacat ggaatcaggg 1000
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 tgcagctatc tctgcctca gccctcaag tagctgggac tacagggtga 1150
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 gccttggcct cccaaagtgc tgggattaca gatgtgagcc accacacctg 1300
 gcccgaagct tgaattttca ttctgccatt gacttggcat ttaccttggg 1350
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 gtagggaaac tgcctctcata ggaaagtttt ctgcttttta aatacaaaaa 2050

tacataaaaa tacataaaat ctgatgatga atataaaaaa gtaaccaacc 2100
tcattggaac aagtattaac attttggaat atgttttatt agttttgtga 2150
tgtactgttt tacaattttt accatttttt tcagtaatta ctgtaaaatg 2200
gtattattgg aatgaaacta tatttcctca tgtgctgatt tgtcttattt 2250
ttttcatact ttcccaactgg tgctattttt atttccaatg gatattttctg 2300
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agaaattgta ccaattttac taaattatgc agttttaaag ggatgatttt 2400
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aaaaaaaaaa aaaaaaaaaa aaaaaaaaa 2478

<210> 477

<211> 201

<212> PRT

<213> Homo sapiens

<400> 477

Met	Glu	Tyr	His	Pro	Asp	Leu	Glu	Asn	Leu	Asp	Glu	Asp	Gly	Tyr	1	5	10	15
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Val	Ser	Glu	Lys	Gly	Ser	Cys	Ala	Ala	Ser	Pro	Pro	Trp	Arg	Leu	35	40	45	
Ile	Ala	Val	Ile	Leu	Gly	Ile	Leu	Cys	Leu	Val	Ile	Leu	Val	Ile	50	55	60	
Ala	Val	Val	Leu	Gly	Thr	Met	Gly	Val	Leu	Ser	Ser	Pro	Cys	Pro	65	70	75	
Pro	Asn	Trp	Ile	Ile	Tyr	Glu	Lys	Ser	Cys	Tyr	Leu	Phe	Ser	Met	80	85	90	
Ser	Leu	Asn	Ser	Trp	Asp	Gly	Ser	Lys	Arg	Gln	Cys	Trp	Gln	Leu	95	100	105	
Gly	Ser	Asn	Leu	Leu	Lys	Ile	Asp	Ser	Ser	Asn	Glu	Leu	Gly	Phe	110	115	120	
Ile	Val	Lys	Gln	Val	Ser	Ser	Gln	Pro	Asp	Asn	Ser	Phe	Trp	Ile	125	130	135	
Gly	Leu	Ser	Arg	Pro	Gln	Thr	Glu	Val	Pro	Trp	Leu	Trp	Glu	Asp	140	145	150	
Gly	Ser	Thr	Phe	Ser	Ser	Asn	Leu	Phe	Gln	Ile	Arg	Thr	Thr	Ala	155	160	165	
Thr	Gln	Glu	Asn	Pro	Ser	Pro	Asn	Cys	Val	Trp	Ile	His	Val	Ser				

	170		175		180
Val Ile Tyr Asp Gln Leu Cys Ser Val Pro Ser Tyr Ser Ile Cys					
	185		190		195
Glu Lys Lys Phe Ser Met					
	200				

<210> 478
 <211> 27
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 478
 gtccacagac agtcattctca ggagcag 27

<210> 479
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 479
 acaagtgtct tcccaacctg 20

<210> 480
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 480
 atcctcccag agccatggta cctc 24

<210> 481
 <211> 51
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 481
 ccaaggatag ctgttggttc agagaaagga tcgtgtgctg catctcctcc 50

t 51

<210> 482
 <211> 3819
 <212> DNA
 <213> Homo sapiens

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<210> 483
 <211> 693
 <212> PRT
 <213> Homo sapiens

<400> 483
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 20 25 30
 Asp Phe Arg Phe Cys Ser Gln Arg Asn Gln Thr His Arg Ser Ser
 35 40 45
 Leu His Tyr Lys Pro Thr Pro Asp Leu Arg Ile Ser Ile Glu Asn
 50 55 60
 Ser Glu Glu Ala Leu Thr Val His Ala Pro Phe Pro Ala Ala His
 65 70 75

Pro	Ala	Ser	Arg	Ser	Phe	Pro	Asp	Pro	Arg	Gly	Leu	Tyr	His	Phe	
				80					85					90	
Cys	Leu	Tyr	Trp	Asn	Arg	His	Ala	Gly	Arg	Leu	His	Leu	Leu	Tyr	
				95					100					105	
Gly	Lys	Arg	Asp	Phe	Leu	Leu	Ser	Asp	Lys	Ala	Ser	Ser	Leu	Leu	
				110					115					120	
Cys	Phe	Gln	His	Gln	Glu	Glu	Ser	Leu	Ala	Gln	Gly	Pro	Pro	Leu	
				125					130					135	
Leu	Ala	Thr	Ser	Val	Thr	Ser	Trp	Trp	Ser	Pro	Gln	Asn	Ile	Ser	
				140					145					150	
Leu	Pro	Ser	Ala	Ala	Ser	Phe	Thr	Phe	Ser	Phe	His	Ser	Pro	Pro	
				155					160					165	
His	Thr	Ala	Ala	His	Asn	Ala	Ser	Val	Asp	Met	Cys	Glu	Leu	Lys	
				170					175					180	
Arg	Asp	Leu	Gln	Leu	Leu	Ser	Gln	Phe	Leu	Lys	His	Pro	Gln	Lys	
				185					190					195	
Ala	Ser	Arg	Arg	Pro	Ser	Ala	Ala	Pro	Ala	Ser	Gln	Gln	Leu	Gln	
				200					205					210	
Ser	Leu	Glu	Ser	Lys	Leu	Thr	Ser	Val	Arg	Phe	Met	Gly	Asp	Met	
				215					220					225	
Val	Ser	Phe	Glu	Glu	Asp	Arg	Ile	Asn	Ala	Thr	Val	Trp	Lys	Leu	
				230					235					240	
Gln	Pro	Thr	Ala	Gly	Leu	Gln	Asp	Leu	His	Ile	His	Ser	Arg	Gln	
				245					250					255	
Glu	Glu	Glu	Gln	Ser	Glu	Ile	Met	Glu	Tyr	Ser	Val	Leu	Leu	Pro	
				260					265					270	
Arg	Thr	Leu	Phe	Gln	Arg	Thr	Lys	Gly	Arg	Ser	Gly	Glu	Ala	Glu	
				275					280					285	
Lys	Arg	Leu	Leu	Leu	Val	Asp	Phe	Ser	Ser	Gln	Ala	Leu	Phe	Gln	
				290					295					300	
Asp	Lys	Asn	Ser	Ser	Gln	Val	Leu	Gly	Glu	Lys	Val	Leu	Gly	Ile	
				305					310					315	
Val	Val	Gln	Asn	Thr	Lys	Val	Ala	Asn	Leu	Thr	Glu	Pro	Val	Val	
				320					325					330	
Leu	Thr	Phe	Gln	His	Gln	Leu	Gln	Pro	Lys	Asn	Val	Thr	Leu	Gln	
				335					340					345	
Cys	Val	Phe	Trp	Val	Glu	Asp	Pro	Thr	Leu	Ser	Ser	Pro	Gly	His	
				350					355					360	
Trp	Ser	Ser	Ala	Gly	Cys	Glu	Thr	Val	Arg	Arg	Glu	Thr	Gln	Thr	

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Ser Cys Phe Cys Asn His Leu Thr Tyr	Phe Ala Val Leu Met Val	
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Ser Ser Val Glu Val Asp Ala Val His	Lys His Tyr Leu Ser Leu	
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Leu Ser Tyr Val Gly Cys Val Val Ser	Ala Leu Ala Cys Leu Val	
410	415	420
Thr Ile Ala Ala Tyr Leu Cys Ser Arg	Val Pro Leu Pro Cys Arg	
425	430	435
Arg Lys Pro Arg Asp Tyr Thr Ile Lys	Val His Met Asn Leu Leu	
440	445	450
Leu Ala Val Phe Leu Leu Asp Thr Ser	Phe Leu Leu Ser Glu Pro	
455	460	465
Val Ala Leu Thr Gly Ser Glu Ala Gly	Cys Arg Ala Ser Ala Ile	
470	475	480
Phe Leu His Phe Ser Leu Leu Thr Cys	Leu Ser Trp Met Gly Leu	
485	490	495
Glu Gly Tyr Asn Leu Tyr Arg Leu Val	Val Glu Val Phe Gly Thr	
500	505	510
Tyr Val Pro Gly Tyr Leu Leu Lys Leu	Ser Ala Met Gly Trp Gly	
515	520	525
Phe Pro Ile Phe Leu Val Thr Leu Val	Ala Leu Val Asp Val Asp	
530	535	540
Asn Tyr Gly Pro Ile Ile Leu Ala Val	His Arg Thr Pro Glu Gly	
545	550	555
Val Ile Tyr Pro Ser Met Cys Trp Ile	Arg Asp Ser Leu Val Ser	
560	565	570
Tyr Ile Thr Asn Leu Gly Leu Phe Ser	Leu Val Phe Leu Phe Asn	
575	580	585
Met Ala Met Leu Ala Thr Met Val Val	Gln Ile Leu Arg Leu Arg	
590	595	600
Pro His Thr Gln Lys Trp Ser His Val	Leu Thr Leu Leu Gly Leu	
605	610	615
Ser Leu Val Leu Gly Leu Pro Trp Ala	Leu Ile Phe Phe Ser Phe	
620	625	630
Ala Ser Gly Thr Phe Gln Leu Val Val	Leu Tyr Leu Phe Ser Ile	
635	640	645
Ile Thr Ser Phe Gln Gly Phe Leu Ile	Phe Ile Trp Tyr Trp Ser	
650	655	660

Met Arg Leu Gln Ala Arg Gly Gly Pro Ser Pro Leu Lys Ser Asn
665 670 675

Ser Asp Ser Ala Arg Leu Pro Ile Ser Ser Gly Ser Thr Ser Ser
680 685 690

Ser Arg Ile

<210> 484
<211> 516
<212> DNA
<213> Homo sapiens

<220>
<221> unsure
<222> 68, 70, 84, 147
<223> unknown base

<400> 484
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ctgctgctgg cagtcttctt gctggacacg agcttcctgc tcagcgnagc 150
cggtggccct gacaggctct gaaggctggc tgccgagcca gtgccatctt 200
cctgcacttc tctgctcac ctgcctttcc tggatgggcc tcgaggggta 250
caacctctac cgactcgtgg tggaggtctt tggcacctat gtccctggct 300
acctactcaa gctgagcgcc atgggctggg gcttccccat ctttctggtg 350
acgctggtgg ccctgggtgga tgtggacaac tatggcccca tcattctggc 400
tgtgcatagg actccagagg gcgtcatcta cccttccatg tgctggatcc 450
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tttctgttca acatgg 516

<210> 485
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 485
ggcattggag cagtgcctgg tg 22

<210> 486
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 486
tggaggccta gatgcggctg gacg 24

<210> 487
<211> 2849
<212> DNA
<213> Homo sapiens

<220>
<221> unsure
<222> 2715
<223> unknown base

<400> 487
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aagagggctc taggaaaaag ttttgatgg gattatgtgg aaactaccct 150
gcgattctct gctgccagag caggctcggc gcttccaccc cagtgcagcc 200
ttcccctggc ggtggtgaaa gagactcggg agtcgctgct tccaaagtgc 250
ccgcgctgag tgagctctca cccagtcag ccaaagtgc ctcttcgggc 300
ttctcctgct gacatctgcc ctggccggcc agagacaggg gactcaggcg 350
gaatccaacc tgagtagtaa attccagttt tccagcaaca aggaacagaa 400
cggagtacaa gatcctcagc atgagagaat tattactgtg tctactaatg 450
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gtttgatgaa agatttgggc ttgaagacc agaagatgac atatgcaagt 600
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tggtgtggtt ctggtactgt accaggaaaa cagatttcta aaggaaatca 700
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<210> 488
 <211> 345
 <212> PRT
 <213> Homo sapiens

<400> 488
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 20 25 30
 Gln Phe Ser Ser Asn Lys Glu Gln Asn Gly Val Gln Asp Pro Gln
 35 40 45
 His Glu Arg Ile Ile Thr Val Ser Thr Asn Gly Ser Ile His Ser
 50 55 60
 Pro Arg Phe Pro His Thr Tyr Pro Arg Asn Thr Val Leu Val Trp
 65 70 75
 Arg Leu Val Ala Val Glu Glu Asn Val Trp Ile Gln Leu Thr Phe
 80 85 90
 Asp Glu Arg Phe Gly Leu Glu Asp Pro Glu Asp Asp Ile Cys Lys
 95 100 105
 Tyr Asp Phe Val Glu Val Glu Glu Pro Ser Asp Gly Thr Ile Leu
 110 115 120
 Gly Arg Trp Cys Gly Ser Gly Thr Val Pro Gly Lys Gln Ile Ser
 125 130 135
 Lys Gly Asn Gln Ile Arg Ile Arg Phe Val Ser Asp Glu Tyr Phe
 140 145 150
 Pro Ser Glu Pro Gly Phe Cys Ile His Tyr Asn Ile Val Met Pro
 155 160 165
 Gln Phe Thr Glu Ala Val Ser Pro Ser Val Leu Pro Pro Ser Ala
 170 175 180
 Leu Pro Leu Asp Leu Leu Asn Asn Ala Ile Thr Ala Phe Ser Thr
 185 190 195

Leu	Glu	Asp	Leu	Ile	Arg	Tyr	Leu	Glu	Pro	Glu	Arg	Trp	Gln	Leu	
				200					205					210	
Asp	Leu	Glu	Asp	Leu	Tyr	Arg	Pro	Thr	Trp	Gln	Leu	Leu	Gly	Lys	
				215					220					225	
Ala	Phe	Val	Phe	Gly	Arg	Lys	Ser	Arg	Val	Val	Asp	Leu	Asn	Leu	
				230					235					240	
Leu	Thr	Glu	Glu	Val	Arg	Leu	Tyr	Ser	Cys	Thr	Pro	Arg	Asn	Phe	
				245					250					255	
Ser	Val	Ser	Ile	Arg	Glu	Glu	Leu	Lys	Arg	Thr	Asp	Thr	Ile	Phe	
				260					265					270	
Trp	Pro	Gly	Cys	Leu	Leu	Val	Lys	Arg	Cys	Gly	Gly	Asn	Cys	Ala	
				275					280					285	
Cys	Cys	Leu	His	Asn	Cys	Asn	Glu	Cys	Gln	Cys	Val	Pro	Ser	Lys	
				290					295					300	
Val	Thr	Lys	Lys	Tyr	His	Glu	Val	Leu	Gln	Leu	Arg	Pro	Lys	Thr	
				305					310					315	
Gly	Val	Arg	Gly	Leu	His	Lys	Ser	Leu	Thr	Asp	Val	Ala	Leu	Glu	
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His	His	Glu	Glu	Cys	Asp	Cys	Val	Cys	Arg	Gly	Ser	Thr	Gly	Gly	
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<210> 489

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 489

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<210> 490

<211> 40

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 490

gaactaaaga gaaccgatac cattttctgg ccaggttgtc 40

<210> 491

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 491

caccacagcg tttaaccagg 20

<210> 492

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 492

acaacaggca cagttccac 20

<210> 493

<211> 21

<212> DNA

<213> Artificial Sequence

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<223> Synthetic oligonucleotide probe

<400> 493

ggcggaatcc aacctgagta g 21

<210> 494

<211> 20

<212> DNA

<213> Artificial Sequence

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<223> Synthetic oligonucleotide probe

<400> 494

gcggctatcc tctgtgctc 20

<210> 495

<211> 3283

<212> DNA

<213> Homo sapiens

<400> 495

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ggacactgaa gagacaaatt cttatccttt ttaacataat cctaatttcc 150

aaactccttg gggctagatg gtttctctaa actctgccct gtgatgtcac 200

tctggatgtt ccaaagaacc atgtgatcgt ggactgcaca gacaagcatt 250

tgacagaaat tcttgagggt attcccacga acaccacgaa cctcaccctc 300

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 aacatagaaa tactctacct gggccaaaac tggtattatc gaaatccttg 650
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 aatccaagaa gatgatttta ataacctcaa ccaattacaa attcttgacc 850
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 atttcttgag aagccctttc agaagtccaa gttcctccag ctccggaaaa 3100
 ggctctgtgg gagttctgtc cttgagtggc caacaaacc gcaagctcac 3150
 ccatacttct ggcagtgtct aaagaacgcc ctggccacag acaatcatgt 3200
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acaactgcct agtttaccaa ggagaggcct ggc 3283

<210> 496

<211> 1049

<212> PRT

<213> Homo sapiens

<400> 496

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				20					25					30

Pro	Lys	Thr	Leu	Pro	Cys	Asp	Val	Thr	Leu	Asp	Val	Pro	Lys	Asn
				35					40					45

His	Val	Ile	Val	Asp	Cys	Thr	Asp	Lys	His	Leu	Thr	Glu	Ile	Pro
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Gly	Gly	Ile	Pro	Thr	Asn	Thr	Thr	Asn	Leu	Thr	Leu	Thr	Ile	Asn
				65					70					75

His	Ile	Pro	Asp	Ile	Ser	Pro	Ala	Ser	Phe	His	Arg	Leu	Asp	His
				80					85					90

Leu	Val	Glu	Ile	Asp	Phe	Arg	Cys	Asn	Cys	Val	Pro	Ile	Pro	Leu
				95					100					105

Gly	Ser	Lys	Asn	Asn	Met	Cys	Ile	Lys	Arg	Leu	Gln	Ile	Lys	Pro
				110					115					120

Arg	Ser	Phe	Ser	Gly	Leu	Thr	Tyr	Leu	Lys	Ser	Leu	Tyr	Leu	Asp
				125					130					135

Gly	Asn	Gln	Leu	Leu	Glu	Ile	Pro	Gln	Gly	Leu	Pro	Pro	Ser	Leu
				140					145					150

Gln	Leu	Leu	Ser	Leu	Glu	Ala	Asn	Asn	Ile	Phe	Ser	Ile	Arg	Lys
				155					160					165

Glu	Asn	Leu	Thr	Glu	Leu	Ala	Asn	Ile	Glu	Ile	Leu	Tyr	Leu	Gly
				170					175					180

Gln	Asn	Cys	Tyr	Tyr	Arg	Asn	Pro	Cys	Tyr	Val	Ser	Tyr	Ser	Ile
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Glu	Lys	Asp	Ala	Phe	Leu	Asn	Leu	Thr	Lys	Leu	Lys	Val	Leu	Ser
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Leu	Lys	Asp	Asn	Asn	Val	Thr	Ala	Val	Pro	Thr	Val	Leu	Pro	Ser
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Thr	Leu	Thr	Glu	Leu	Tyr	Leu	Tyr	Asn	Asn	Met	Ile	Ala	Lys	Ile
				230					235					240

Gln	Glu	Asp	Asp	Phe	Asn	Asn	Leu	Asn	Gln	Leu	Gln	Ile	Leu	Asp
				245					250					255

Leu	Ser	Gly	Asn	Cys	Pro	Arg	Cys	Tyr	Asn	Ala	Pro	Phe	Pro	Cys	
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Ala	Pro	Cys	Lys	Asn	Asn	Ser	Pro	Leu	Gln	Ile	Pro	Val	Asn	Ala	
				275					280					285	
Phe	Asp	Ala	Leu	Thr	Glu	Leu	Lys	Val	Leu	Arg	Leu	His	Ser	Asn	
				290					295					300	
Ser	Leu	Gln	His	Val	Pro	Pro	Arg	Trp	Phe	Lys	Asn	Ile	Asn	Lys	
				305					310					315	
Leu	Gln	Glu	Leu	Asp	Leu	Ser	Gln	Asn	Phe	Leu	Ala	Lys	Glu	Ile	
				320					325					330	
Gly	Asp	Ala	Lys	Phe	Leu	His	Phe	Leu	Pro	Ser	Leu	Ile	Gln	Leu	
				335					340					345	
Asp	Leu	Ser	Phe	Asn	Phe	Glu	Leu	Gln	Val	Tyr	Arg	Ala	Ser	Met	
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Asn	Leu	Ser	Gln	Ala	Phe	Ser	Ser	Leu	Lys	Ser	Leu	Lys	Ile	Leu	
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Arg	Ile	Arg	Gly	Tyr	Val	Phe	Lys	Glu	Leu	Lys	Ser	Phe	Asn	Leu	
				380					385					390	
Ser	Pro	Leu	His	Asn	Leu	Gln	Asn	Leu	Glu	Val	Leu	Asp	Leu	Gly	
				395					400					405	
Thr	Asn	Phe	Ile	Lys	Ile	Ala	Asn	Leu	Ser	Met	Phe	Lys	Gln	Phe	
				410					415					420	
Lys	Arg	Leu	Lys	Val	Ile	Asp	Leu	Ser	Val	Asn	Lys	Ile	Ser	Pro	
				425					430					435	
Ser	Gly	Asp	Ser	Ser	Glu	Val	Gly	Phe	Cys	Ser	Asn	Ala	Arg	Thr	
				440					445					450	
Ser	Val	Glu	Ser	Tyr	Glu	Pro	Gln	Val	Leu	Glu	Gln	Leu	His	Tyr	
				455					460					465	
Phe	Arg	Tyr	Asp	Lys	Tyr	Ala	Arg	Ser	Cys	Arg	Phe	Lys	Asn	Lys	
				470					475					480	
Glu	Ala	Ser	Phe	Met	Ser	Val	Asn	Glu	Ser	Cys	Tyr	Lys	Tyr	Gly	
				485					490					495	
Gln	Thr	Leu	Asp	Leu	Ser	Lys	Asn	Ser	Ile	Phe	Phe	Val	Lys	Ser	
				500					505					510	
Ser	Asp	Phe	Gln	His	Leu	Ser	Phe	Leu	Lys	Cys	Leu	Asn	Leu	Ser	
				515					520					525	
Gly	Asn	Leu	Ile	Ser	Gln	Thr	Leu	Asn	Gly	Ser	Glu	Phe	Gln	Pro	
				530					535					540	
Leu	Ala	Glu	Leu	Arg	Tyr	Leu	Asp	Phe	Ser	Asn	Asn	Arg	Leu	Asp	

545	550	555
Leu Leu His Ser Thr Ala Phe Glu Glu	Leu His Lys Leu Glu Val	
560	565	570
Leu Asp Ile Ser Ser Asn Ser His Tyr	Phe Gln Ser Glu Gly Ile	
575	580	585
Thr His Met Leu Asn Phe Thr Lys Asn	Leu Lys Val Leu Gln Lys	
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Leu Met Met Asn Asp Asn Asp Ile Ser	Ser Ser Thr Ser Arg Thr	
605	610	615
Met Glu Ser Glu Ser Leu Arg Thr Leu	Glu Phe Arg Gly Asn His	
620	625	630
Leu Asp Val Leu Trp Arg Glu Gly Asp	Asn Arg Tyr Leu Gln Leu	
635	640	645
Phe Lys Asn Leu Leu Lys Leu Glu Glu	Leu Asp Ile Ser Lys Asn	
650	655	660
Ser Leu Ser Phe Leu Pro Ser Gly Val	Phe Asp Gly Met Pro Pro	
665	670	675
Asn Leu Lys Asn Leu Ser Leu Ala Lys	Asn Gly Leu Lys Ser Phe	
680	685	690
Ser Trp Lys Lys Leu Gln Cys Leu Lys	Asn Leu Glu Thr Leu Asp	
695	700	705
Leu Ser His Asn Gln Leu Thr Thr Val	Pro Glu Arg Leu Ser Asn	
710	715	720
Cys Ser Arg Ser Leu Lys Asn Leu Ile	Leu Lys Asn Asn Gln Ile	
725	730	735
Arg Ser Leu Thr Lys Tyr Phe Leu Gln	Asp Ala Phe Gln Leu Arg	
740	745	750
Tyr Leu Asp Leu Ser Ser Asn Lys Ile	Gln Met Ile Gln Lys Thr	
755	760	765
Ser Phe Pro Glu Asn Val Leu Asn Asn	Leu Lys Met Leu Leu Leu	
770	775	780
His His Asn Arg Phe Leu Cys Thr Cys	Asp Ala Val Trp Phe Val	
785	790	795
Trp Trp Val Asn His Thr Glu Val Thr	Ile Pro Tyr Leu Ala Thr	
800	805	810
Asp Val Thr Cys Val Gly Pro Gly Ala	His Lys Gly Gln Ser Val	
815	820	825
Ile Ser Leu Asp Leu Tyr Thr Cys Glu	Leu Asp Leu Thr Asn Leu	
830	835	840

Ile	Leu	Phe	Ser	Leu	Ser	Ile	Ser	Val	Ser	Leu	Phe	Leu	Met	Val
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Met	Met	Thr	Ala	Ser	His	Leu	Tyr	Phe	Trp	Asp	Val	Trp	Tyr	Ile
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Tyr	His	Phe	Cys	Lys	Ala	Lys	Ile	Lys	Gly	Tyr	Gln	Arg	Leu	Ile
				875					880					885
Ser	Pro	Asp	Cys	Cys	Tyr	Asp	Ala	Phe	Ile	Val	Tyr	Asp	Thr	Lys
				890					895					900
Asp	Pro	Ala	Val	Thr	Glu	Trp	Val	Leu	Ala	Glu	Leu	Val	Ala	Lys
				905					910					915
Leu	Glu	Asp	Pro	Arg	Glu	Lys	His	Phe	Asn	Leu	Cys	Leu	Glu	Glu
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Arg	Asp	Trp	Leu	Pro	Gly	Gln	Pro	Val	Leu	Glu	Asn	Leu	Ser	Gln
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Ser	Ile	Gln	Leu	Ser	Lys	Lys	Thr	Val	Phe	Val	Met	Thr	Asp	Lys
				950					955					960
Tyr	Ala	Lys	Thr	Glu	Asn	Phe	Lys	Ile	Ala	Phe	Tyr	Leu	Ser	His
				965					970					975
Gln	Arg	Leu	Met	Asp	Glu	Lys	Val	Asp	Val	Ile	Ile	Leu	Ile	Phe
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Leu	Glu	Lys	Pro	Phe	Gln	Lys	Ser	Lys	Phe	Leu	Gln	Leu	Arg	Lys
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Arg	Leu	Cys	Gly	Ser	Ser	Val	Leu	Glu	Trp	Pro	Thr	Asn	Pro	Gln
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Ala	His	Pro	Tyr	Phe	Trp	Gln	Cys	Leu	Lys	Asn	Ala	Leu	Ala	Thr
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<210> 497

<211> 4199

<212> DNA

<213> Homo sapiens

<400> 497

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<400> 498
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 35 40 45
 Ile Ala Glu Cys Ser Asn Arg Arg Leu Gln Glu Val Pro Gln Thr

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Val	Gly	Lys	Tyr	Val 65	Thr	Glu	Leu	Asp	Leu 70	Ser	Asp	Asn	Phe	Ile 75
Thr	His	Ile	Thr	Asn 80	Glu	Ser	Phe	Gln	Gly 85	Leu	Gln	Asn	Leu	Thr 90
Lys	Ile	Asn	Leu	Asn 95	His	Asn	Pro	Asn	Val 100	Gln	His	Gln	Asn	Gly 105
Asn	Pro	Gly	Ile	Gln 110	Ser	Asn	Gly	Leu	Asn 115	Ile	Thr	Asp	Gly	Ala 120
Phe	Leu	Asn	Leu	Lys 125	Asn	Leu	Arg	Glu	Leu 130	Leu	Leu	Glu	Asp	Asn 135
Gln	Leu	Pro	Gln	Ile 140	Pro	Ser	Gly	Leu	Pro 145	Glu	Ser	Leu	Thr	Glu 150
Leu	Ser	Leu	Ile	Gln 155	Asn	Asn	Ile	Tyr	Asn 160	Ile	Thr	Lys	Glu	Gly 165
Ile	Ser	Arg	Leu	Ile 170	Asn	Leu	Lys	Asn	Leu 175	Tyr	Leu	Ala	Trp	Asn 180
Cys	Tyr	Phe	Asn	Lys 185	Val	Cys	Glu	Lys	Thr 190	Asn	Ile	Glu	Asp	Gly 195
Val	Phe	Glu	Thr	Leu 200	Thr	Asn	Leu	Glu	Leu 205	Leu	Ser	Leu	Ser	Phe 210
Asn	Ser	Leu	Ser	His 215	Val	Pro	Pro	Lys	Leu 220	Pro	Ser	Ser	Leu	Arg 225
Lys	Leu	Phe	Leu	Ser 230	Asn	Thr	Gln	Ile	Lys 235	Tyr	Ile	Ser	Glu	Glu 240
Asp	Phe	Lys	Gly	Leu 245	Ile	Asn	Leu	Thr	Leu 250	Leu	Asp	Leu	Ser	Gly 255
Asn	Cys	Pro	Arg	Cys 260	Phe	Asn	Ala	Pro	Phe 265	Pro	Cys	Val	Pro	Cys 270
Asp	Gly	Gly	Ala	Ser 275	Ile	Asn	Ile	Asp	Arg 280	Phe	Ala	Phe	Gln	Asn 285
Leu	Thr	Gln	Leu	Arg 290	Tyr	Leu	Asn	Leu	Ser 295	Ser	Thr	Ser	Leu	Arg 300
Lys	Ile	Asn	Ala	Ala 305	Trp	Phe	Lys	Asn	Met 310	Pro	His	Leu	Lys	Val 315
Leu	Asp	Leu	Glu	Phe 320	Asn	Tyr	Leu	Val	Gly 325	Glu	Ile	Val	Ser	Gly 330
Ala	Phe	Leu	Thr	Met 335	Leu	Pro	Arg	Leu	Glu 340	Ile	Leu	Asp	Leu	Ser 345

Phe	Asn	Tyr	Ile	Lys	Gly	Ser	Tyr	Pro	Gln	His	Ile	Asn	Ile	Ser	350	355	360
Arg	Asn	Phe	Ser	Lys	Leu	Leu	Ser	Leu	Arg	Ala	Leu	His	Leu	Arg	365	370	375
Gly	Tyr	Val	Phe	Gln	Glu	Leu	Arg	Glu	Asp	Asp	Phe	Gln	Pro	Leu	380	385	390
Met	Gln	Leu	Pro	Asn	Leu	Ser	Thr	Ile	Asn	Leu	Gly	Ile	Asn	Phe	395	400	405
Ile	Lys	Gln	Ile	Asp	Phe	Lys	Leu	Phe	Gln	Asn	Phe	Ser	Asn	Leu	410	415	420
Glu	Ile	Ile	Tyr	Leu	Ser	Glu	Asn	Arg	Ile	Ser	Pro	Leu	Val	Lys	425	430	435
Asp	Thr	Arg	Gln	Ser	Tyr	Ala	Asn	Ser	Ser	Ser	Phe	Gln	Arg	His	440	445	450
Ile	Arg	Lys	Arg	Arg	Ser	Thr	Asp	Phe	Glu	Phe	Asp	Pro	His	Ser	455	460	465
Asn	Phe	Tyr	His	Phe	Thr	Arg	Pro	Leu	Ile	Lys	Pro	Gln	Cys	Ala	470	475	480
Ala	Tyr	Gly	Lys	Ala	Leu	Asp	Leu	Ser	Leu	Asn	Ser	Ile	Phe	Phe	485	490	495
Ile	Gly	Pro	Asn	Gln	Phe	Glu	Asn	Leu	Pro	Asp	Ile	Ala	Cys	Leu	500	505	510
Asn	Leu	Ser	Ala	Asn	Ser	Asn	Ala	Gln	Val	Leu	Ser	Gly	Thr	Glu	515	520	525
Phe	Ser	Ala	Ile	Pro	His	Val	Lys	Tyr	Leu	Asp	Leu	Thr	Asn	Asn	530	535	540
Arg	Leu	Asp	Phe	Asp	Asn	Ala	Ser	Ala	Leu	Thr	Glu	Leu	Ser	Asp	545	550	555
Leu	Glu	Val	Leu	Asp	Leu	Ser	Tyr	Asn	Ser	His	Tyr	Phe	Arg	Ile	560	565	570
Ala	Gly	Val	Thr	His	His	Leu	Glu	Phe	Ile	Gln	Asn	Phe	Thr	Asn	575	580	585
Leu	Lys	Val	Leu	Asn	Leu	Ser	His	Asn	Asn	Ile	Tyr	Thr	Leu	Thr	590	595	600
Asp	Lys	Tyr	Asn	Leu	Glu	Ser	Lys	Ser	Leu	Val	Glu	Leu	Val	Phe	605	610	615
Ser	Gly	Asn	Arg	Leu	Asp	Ile	Leu	Trp	Asn	Asp	Asp	Asp	Asn	Arg	620	625	630
Tyr	Ile	Ser	Ile	Phe	Lys	Gly	Leu	Lys	Asn	Leu	Thr	Arg	Leu	Asp			

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Asn Leu Pro Ala Ser Leu Thr Glu Leu	His Ile Asn Asp Asn Met	
665	670	675
Leu Lys Phe Phe Asn Trp Thr Leu Leu	Gln Gln Phe Pro Arg Leu	
680	685	690
Glu Leu Leu Asp Leu Arg Gly Asn Lys	Leu Leu Phe Leu Thr Asp	
695	700	705
Ser Leu Ser Asp Phe Thr Ser Ser Leu	Arg Thr Leu Leu Leu Ser	
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725	730	735
Ser Ser Leu Lys His Leu Asp Leu Ser	Ser Asn Leu Leu Lys Thr	
740	745	750
Ile Asn Lys Ser Ala Leu Glu Thr Lys	Thr Thr Thr Lys Leu Ser	
755	760	765
Met Leu Glu Leu His Gly Asn Pro Phe	Glu Cys Thr Cys Asp Ile	
770	775	780
Gly Asp Phe Arg Arg Trp Met Asp Glu	His Leu Asn Val Lys Ile	
785	790	795
Pro Arg Leu Val Asp Val Ile Cys Ala	Ser Pro Gly Asp Gln Arg	
800	805	810
Gly Lys Ser Ile Val Ser Leu Glu Leu	Thr Thr Cys Val Ser Asp	
815	820	825
Val Thr Ala Val Ile Leu Phe Phe Phe	Thr Phe Phe Ile Thr Thr	
830	835	840
Met Val Met Leu Ala Ala Leu Ala His	His Leu Phe Tyr Trp Asp	
845	850	855
Val Trp Phe Ile Tyr Asn Val Cys Leu	Ala Lys Val Lys Gly Tyr	
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Arg Ser Leu Ser Thr Ser Gln Thr Phe	Tyr Asp Ala Tyr Ile Ser	
875	880	885
Tyr Asp Thr Lys Asp Ala Ser Val Thr	Asp Trp Val Ile Asn Glu	
890	895	900
Leu Arg Tyr His Leu Glu Glu Ser Arg	Asp Lys Asn Val Leu Leu	
905	910	915
Cys Leu Glu Glu Arg Asp Trp Asp Pro	Gly Leu Ala Ile Ile Asp	
920	925	930

Asn Leu Met Gln Ser Ile Asn Gln Ser Lys Lys Thr Val Phe Val
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 Tyr Leu Ala Leu Gln Arg Leu Met Asp Glu Asn Met Asp Val Ile
 965 970 975
 Ile Phe Ile Leu Leu Glu Pro Val Leu Gln His Ser Gln Tyr Leu
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 <213> Artificial Sequence

<220>
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<210> 500
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<220>
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<400> 500
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<210> 501
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 <212> DNA
 <213> Artificial Sequence

<220>
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<213> Artificial Sequence

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<212> DNA
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<220>
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<400> 503
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<213> Artificial Sequence

<220>
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<210> 505
<211> 1738
<212> DNA
<213> Homo sapiens

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Cys	Ala	Val	Arg	Ala	His	Gly	Asp	Pro	Val	Ser	Glu	Ser	Phe	Val	35	40	45
Gln	Arg	Val	Tyr	Gln	Pro	Phe	Leu	Thr	Thr	Cys	Asp	Gly	His	Arg	50	55	60
Ala	Cys	Ser	Thr	Tyr	Arg	Thr	Ile	Tyr	Arg	Thr	Ala	Tyr	Arg	Arg	65	70	75
Ser	Pro	Gly	Leu	Ala	Pro	Ala	Arg	Pro	Arg	Tyr	Ala	Cys	Cys	Pro	80	85	90
Gly	Trp	Lys	Arg	Thr	Ser	Gly	Leu	Pro	Gly	Ala	Cys	Gly	Ala	Ala	95	100	105
Ile	Cys	Gln	Pro	Pro	Cys	Arg	Asn	Gly	Gly	Ser	Cys	Val	Gln	Pro	110	115	120
Gly	Arg	Cys	Arg	Cys	Pro	Ala	Gly	Trp	Arg	Gly	Asp	Thr	Cys	Gln	125	130	135
Ser	Asp	Val	Asp	Glu	Cys	Ser	Ala	Arg	Arg	Gly	Gly	Cys	Pro	Gln	140	145	150
Arg	Cys	Ile	Asn	Thr	Ala	Gly	Ser	Tyr	Trp	Cys	Gln	Cys	Trp	Glu	155	160	165
Gly	His	Ser	Leu	Ser	Ala	Asp	Gly	Thr	Leu	Cys	Val	Pro	Lys	Gly	170	175	180
Gly	Pro	Pro	Arg	Val	Ala	Pro	Asn	Pro	Thr	Gly	Val	Asp	Ser	Ala	185	190	195
Met	Lys	Glu	Glu	Val	Gln	Arg	Leu	Gln	Ser	Arg	Val	Asp	Leu	Leu	200	205	210
Glu	Glu	Lys	Leu	Gln	Leu	Val	Leu	Ala	Pro	Leu	His	Ser	Leu	Ala	215	220	225
Ser	Gln	Ala	Leu	Glu	His	Gly	Leu	Pro	Asp	Pro	Gly	Ser	Leu	Leu	230	235	240
Val	His	Ser	Phe	Gln	Gln	Leu	Gly	Arg	Ile	Asp	Ser	Leu	Ser	Glu	245	250	255
Gln	Ile	Ser	Phe	Leu	Glu	Glu	Gln	Leu	Gly	Ser	Cys	Ser	Cys	Lys	260	265	270
Lys	Asp	Ser															

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 <212> DNA
 <213> Homo sapiens

<400> 507

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cgccctgcgg tgtcccagg gctgaggtct cctcatcttc tccctagcag 250
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<210> 508
<211> 273
<212> PRT
<213> Homo sapiens

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Cys Ala Val Arg Ala His Gly Asp Pro Val Ser Glu Ser Phe Val
35 40 45
Gln Arg Val Tyr Gln Pro Phe Leu Thr Thr Cys Asp Gly His Arg
50 55 60
Ala Cys Ser Thr Tyr Arg Thr Ile Tyr Arg Thr Ala Tyr Arg Arg
65 70 75
Ser Pro Gly Leu Ala Pro Ala Arg Pro Arg Tyr Ala Cys Cys Pro
80 85 90
Gly Trp Lys Arg Thr Ser Gly Leu Pro Gly Ala Cys Gly Ala Ala
95 100 105
Ile Cys Gln Pro Pro Cys Arg Asn Gly Gly Ser Cys Val Gln Pro
110 115 120
Gly Arg Cys Arg Cys Pro Ala Gly Trp Arg Gly Asp Thr Cys Gln
125 130 135
Ser Asp Val Asp Glu Cys Ser Ala Arg Arg Gly Gly Cys Pro Gln
140 145 150
Arg Cys Ile Asn Thr Ala Gly Ser Tyr Trp Cys Gln Cys Trp Glu
155 160 165
Gly His Ser Leu Ser Ala Asp Gly Thr Leu Cys Val Pro Lys Gly
170 175 180
Gly Pro Pro Arg Val Ala Pro Asn Pro Thr Gly Val Asp Ser Ala
185 190 195
Met Lys Glu Glu Val Gln Arg Leu Gln Ser Arg Val Asp Leu Leu
200 205 210

10046177-106501

Glu	Glu	Lys	Leu	Gln	Leu	Val	Leu	Ala	Pro	Leu	His	Ser	Leu	Ala
				215					220					225
Ser	Gln	Ala	Leu	Glu	His	Gly	Leu	Pro	Asp	Pro	Gly	Ser	Leu	Leu
				230					235					240
Val	His	Ser	Phe	Gln	Gln	Leu	Gly	Arg	Ile	Asp	Ser	Leu	Ser	Glu
				245					250					255
Gln	Ile	Ser	Phe	Leu	Glu	Glu	Gln	Leu	Gly	Ser	Cys	Ser	Cys	Lys
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Lys Asp Ser

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 <211> 1538
 <212> DNA
 <213> Homo sapiens

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<210> 510
 <211> 273
 <212> PRT
 <213> Homo sapiens

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 20 25 30
 Cys Ala Val Arg Ala His Gly Asp Pro Val Ser Glu Ser Phe Val
 35 40 45
 Gln Arg Val Tyr Gln Pro Phe Leu Thr Thr Cys Asp Gly His Arg
 50 55 60
 Ala Cys Ser Thr Tyr Arg Thr Ile Tyr Arg Thr Ala Tyr Arg Arg
 65 70 75
 Ser Pro Gly Leu Ala Pro Ala Arg Pro Arg Tyr Ala Cys Cys Pro
 80 85 90
 Gly Trp Lys Arg Thr Ser Gly Leu Pro Gly Ala Cys Gly Ala Ala
 95 100 105
 Ile Cys Gln Pro Pro Cys Arg Asn Gly Gly Ser Cys Val Gln Pro
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<400> 513
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<210> 514
<211> 2690
<212> DNA
<213> Homo sapiens

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<221> unsure
<222> 2039-2065
<223> unknown base

<400> 514
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<210> 515
<211> 364
<212> PRT
<213> Homo sapiens

<400> 515
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35 40 45
Leu Gly Thr Cys Thr Leu Phe Phe Ala Phe Glu Cys Arg Tyr Leu
50 55 60
Ala Val Gln Leu Ser Pro Ala Ile Pro Val Phe Ala Ala Met Leu
65 70 75
Phe Leu Phe Ser Met Ala Thr Leu Leu Arg Thr Ser Phe Ser Asp
80 85 90
Pro Gly Val Ile Pro Arg Ala Leu Pro Asp Glu Ala Ala Phe Ile
95 100 105
Glu Met Glu Ile Glu Ala Thr Asn Gly Ala Val Pro Gln Gly Gln
110 115 120
Arg Pro Pro Pro Arg Ile Lys Asn Phe Gln Ile Asn Asn Gln Ile
125 130 135
Val Lys Leu Lys Tyr Cys Tyr Thr Cys Lys Ile Phe Arg Pro Pro
140 145 150
Arg Ala Ser His Cys Ser Ile Cys Asp Asn Cys Val Glu Arg Phe
155 160 165
Asp His His Cys Pro Trp Val Gly Asn Cys Val Gly Lys Arg Asn
170 175 180
Tyr Arg Tyr Phe Tyr Leu Phe Ile Leu Ser Leu Ser Leu Leu Thr
185 190 195
Ile Tyr Val Phe Ala Phe Asn Ile Val Tyr Val Ala Leu Lys Ser
200 205 210
Leu Lys Ile Gly Phe Leu Glu Thr Leu Lys Glu Thr Pro Gly Thr
215 220 225
Val Leu Glu Val Leu Ile Cys Phe Phe Thr Leu Trp Ser Val Val

100467.406604

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	260	265		270	
Gln Asn Pro Tyr	Ser His Gly Asn Ile	Val Lys Asn Cys Cys Glu			
	275	280		285	
Val Leu Cys Gly	Pro Leu Pro Pro Ser	Val Leu Asp Arg Arg Gly			
	290	295		300	
Ile Leu Pro Leu	Glu Glu Ser Gly Ser	Arg Pro Pro Ser Thr Gln			
	305	310		315	
Glu Thr Ser Ser	Ser Leu Leu Pro Gln	Ser Pro Ala Pro Thr Glu			
	320	325		330	
His Leu Asn Ser	Asn Glu Met Pro Glu	Asp Ser Ser Thr Pro Glu			
	335	340		345	
Glu Met Pro Pro	Pro Glu Pro Pro Glu	Pro Pro Gln Glu Ala Ala			
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Glu Ala Glu Lys					

<210> 516
 <211> 255
 <212> DNA
 <213> Homo sapiens

<220>
 <221> unsure
 <222> 36, 38, 88, 118, 135, 193, 213, 222
 <223> unknown base

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 cccctgggtg gggaattgtg ttggaaagag gaactaccgc tanttttacc 200
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 atcgt 255

<210> 517
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 517

caacgtgatt tcaaagctgg gctc 24

<210> 518

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 518

gcctcgtatc aagaatttcc 20

<210> 519

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 519

agtggaagtc gacctccc 18

<210> 520

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 520

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<210> 521

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 521

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<210> 522

<211> 1679

<212> DNA

<213> Homo sapiens

<400> 522

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aattcaatca gtccatagag acgaacagaa tgagaccttc cggcccaagc 1600
 gtggcgctgc gggcactttg gtagactgtg ccaccacggc gtgtgttgtg 1650
 aaacgtgaaa taaaaagagc aaaaaaaaaa 1679

<210> 523
 <211> 344
 <212> PRT
 <213> Homo sapiens

<400> 523
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 35 40 45
 Thr Val Arg Gln Gly Glu Ser Ala Thr Leu Arg Cys Thr Ile Asp
 50 55 60
 Asn Arg Val Thr Arg Val Ala Trp Leu Asn Arg Ser Thr Ile Leu
 65 70 75
 Tyr Ala Gly Asn Asp Lys Trp Cys Leu Asp Pro Arg Val Val Leu
 80 85 90
 Leu Ser Asn Thr Gln Thr Gln Tyr Ser Ile Glu Ile Gln Asn Val
 95 100 105
 Asp Val Tyr Asp Glu Gly Pro Tyr Thr Cys Ser Val Gln Thr Asp
 110 115 120
 Asn His Pro Lys Thr Ser Arg Val His Leu Ile Val Gln Val Ser
 125 130 135
 Pro Lys Ile Val Glu Ile Ser Ser Asp Ile Ser Ile Asn Glu Gly
 140 145 150
 Asn Asn Ile Ser Leu Thr Cys Ile Ala Thr Gly Arg Pro Glu Pro
 155 160 165
 Thr Val Thr Trp Arg His Ile Ser Pro Lys Ala Val Gly Phe Val
 170 175 180
 Ser Glu Asp Glu Tyr Leu Glu Ile Gln Gly Ile Thr Arg Glu Gln
 185 190 195
 Ser Gly Asp Tyr Glu Cys Ser Ala Ser Asn Asp Val Ala Ala Pro
 200 205 210
 Val Val Arg Arg Val Lys Val Thr Val Asn Tyr Pro Pro Tyr Ile
 215 220 225
 Ser Glu Ala Lys Gly Thr Gly Val Pro Val Gly Gln Lys Gly Thr

230	235	240
Leu Gln Cys Glu Ala Ser Ala Val Pro Ser Ala Glu Phe Gln Trp		
245	250	255
Tyr Lys Asp Asp Lys Arg Leu Ile Glu Gly Lys Lys Gly Val Lys		
260	265	270
Val Glu Asn Arg Pro Phe Leu Ser Lys Leu Ile Phe Phe Asn Val		
275	280	285
Ser Glu His Asp Tyr Gly Asn Tyr Thr Cys Val Ala Ser Asn Lys		
290	295	300
Leu Gly His Thr Asn Ala Ser Ile Met Leu Phe Gly Pro Gly Ala		
305	310	315
Val Ser Glu Val Ser Asn Gly Thr Ser Arg Arg Ala Gly Cys Val		
320	325	330
Trp Leu Leu Pro Leu Leu Val Leu His Leu Leu Leu Lys Phe		
335	340	

<210> 524
 <211> 503
 <212> DNA
 <213> Homo sapiens

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 acccggtggtg cctggctaaa ccgcagcacc atcctctatg ctgggaatga 250
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 gag 503

<210> 525
 <211> 2602
 <212> DNA
 <213> Homo sapiens

<400> 525
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 cc 2602

<210> 526
 <211> 736
 <212> PRT
 <213> Homo sapiens

<400> 526
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 Phe Gln Lys Gly Thr Arg Gln Leu Leu Gly Ser Arg Thr Gln Leu
 20 25 30

Glu	Leu	Val	Leu	Ala	Gly	Ala	Ser	Leu	Leu	Leu	Ala	Ala	Leu	Leu	35	40	45
Leu	Gly	Cys	Leu	Val	Ala	Leu	Gly	Val	Gln	Tyr	His	Arg	Asp	Pro	50	55	60
Ser	His	Ser	Thr	Cys	Leu	Thr	Glu	Ala	Cys	Ile	Arg	Val	Ala	Gly	65	70	75
Lys	Ile	Leu	Glu	Ser	Leu	Asp	Arg	Gly	Val	Ser	Pro	Cys	Glu	Asp	80	85	90
Phe	Tyr	Gln	Phe	Ser	Cys	Gly	Gly	Trp	Ile	Arg	Arg	Asn	Pro	Leu	95	100	105
Pro	Asp	Gly	Arg	Ser	Arg	Trp	Asn	Thr	Phe	Asn	Ser	Leu	Trp	Asp	110	115	120
Gln	Asn	Gln	Ala	Ile	Leu	Lys	His	Leu	Leu	Glu	Asn	Thr	Thr	Phe	125	130	135
Asn	Ser	Ser	Ser	Glu	Ala	Glu	Gln	Lys	Thr	Gln	Arg	Phe	Tyr	Leu	140	145	150
Ser	Cys	Leu	Gln	Val	Glu	Arg	Ile	Glu	Glu	Leu	Gly	Ala	Gln	Pro	155	160	165
Leu	Arg	Asp	Leu	Ile	Glu	Lys	Ile	Gly	Gly	Trp	Asn	Ile	Thr	Gly	170	175	180
Pro	Trp	Asp	Gln	Asp	Asn	Phe	Met	Glu	Val	Leu	Lys	Ala	Val	Ala	185	190	195
Gly	Thr	Tyr	Arg	Ala	Thr	Pro	Phe	Phe	Thr	Val	Tyr	Ile	Ser	Ala	200	205	210
Asp	Ser	Lys	Ser	Ser	Asn	Ser	Asn	Val	Ile	Gln	Val	Asp	Gln	Ser	215	220	225
Gly	Leu	Phe	Leu	Pro	Ser	Arg	Asp	Tyr	Tyr	Leu	Asn	Arg	Thr	Ala	230	235	240
Asn	Glu	Lys	Val	Leu	Thr	Ala	Tyr	Leu	Asp	Tyr	Met	Glu	Glu	Leu	245	250	255
Gly	Met	Leu	Leu	Gly	Gly	Arg	Pro	Thr	Ser	Thr	Arg	Glu	Gln	Met	260	265	270
Gln	Gln	Val	Leu	Glu	Leu	Glu	Ile	Gln	Leu	Ala	Asn	Ile	Thr	Val	275	280	285
Pro	Gln	Asp	Gln	Arg	Arg	Asp	Glu	Glu	Lys	Ile	Tyr	His	Lys	Met	290	295	300
Ser	Ile	Ser	Glu	Leu	Gln	Ala	Leu	Ala	Pro	Ser	Met	Asp	Trp	Leu	305	310	315
Glu	Phe	Leu	Ser	Phe	Leu	Leu	Ser	Pro	Leu	Glu	Leu	Ser	Asp	Ser			

320	325	330
Glu Pro Val Val Val Tyr Gly Met Asp Tyr Leu Gln Gln Val Ser		
335	340	345
Glu Leu Ile Asn Arg Thr Glu Pro Ser Ile Leu Asn Asn Tyr Leu		
350	355	360
Ile Trp Asn Leu Val Gln Lys Thr Thr Ser Ser Leu Asp Arg Arg		
365	370	375
Phe Glu Ser Ala Gln Glu Lys Leu Leu Glu Thr Leu Tyr Gly Thr		
380	385	390
Lys Lys Ser Cys Val Pro Arg Trp Gln Thr Cys Ile Ser Asn Thr		
395	400	405
Asp Asp Ala Leu Gly Phe Ala Leu Gly Ser Leu Phe Val Lys Ala		
410	415	420
Thr Phe Asp Arg Gln Ser Lys Glu Ile Ala Glu Gly Met Ile Ser		
425	430	435
Glu Ile Arg Thr Ala Phe Glu Glu Ala Leu Gly Gln Leu Val Trp		
440	445	450
Met Asp Glu Lys Thr Arg Gln Ala Ala Lys Glu Lys Ala Asp Ala		
455	460	465
Ile Tyr Asp Met Ile Gly Phe Pro Asp Phe Ile Leu Glu Pro Lys		
470	475	480
Glu Leu Asp Asp Val Tyr Asp Gly Tyr Glu Ile Ser Glu Asp Ser		
485	490	495
Phe Phe Gln Asn Met Leu Asn Leu Tyr Asn Phe Ser Ala Lys Val		
500	505	510
Met Ala Asp Gln Leu Arg Lys Pro Pro Ser Arg Asp Gln Trp Ser		
515	520	525
Met Thr Pro Gln Thr Val Asn Ala Tyr Tyr Leu Pro Thr Lys Asn		
530	535	540
Glu Ile Val Phe Pro Ala Gly Ile Leu Gln Ala Pro Phe Tyr Ala		
545	550	555
Arg Asn His Pro Lys Ala Leu Asn Phe Gly Gly Ile Gly Val Val		
560	565	570
Met Gly His Glu Leu Thr His Ala Phe Asp Asp Gln Gly Arg Glu		
575	580	585
Tyr Asp Lys Glu Gly Asn Leu Arg Pro Trp Trp Gln Asn Glu Ser		
590	595	600
Leu Ala Ala Phe Arg Asn His Thr Ala Cys Met Glu Glu Gln Tyr		
605	610	615

Asn	Gln	Tyr	Gln	Val	Asn	Gly	Glu	Arg	Leu	Asn	Gly	Arg	Gln	Thr
				620					625					630
Leu	Gly	Glu	Asn	Ile	Thr	Asp	Asn	Gly	Gly	Leu	Lys	Ala	Ala	Tyr
				635					640					645
Asn	Ala	Tyr	Lys	Ala	Trp	Leu	Arg	Lys	His	Gly	Glu	Glu	Gln	Gln
				650					655					660
Leu	Pro	Ala	Val	Gly	Leu	Thr	Asn	His	Gln	Leu	Phe	Phe	Val	Gly
				665					670					675
Phe	Ala	Gln	Val	Trp	Cys	Ser	Val	Arg	Thr	Pro	Glu	Ser	Ser	His
				680					685					690
Glu	Gly	Leu	Val	Thr	Asp	Pro	His	Ser	Pro	Ala	Arg	Phe	Arg	Val
				695					700					705
Leu	Gly	Thr	Leu	Ser	Asn	Ser	Arg	Asp	Phe	Leu	Arg	His	Phe	Gly
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Cys	Pro	Val	Gly	Ser	Pro	Met	Asn	Pro	Gly	Gln	Leu	Cys	Glu	Val
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Trp

<210> 527
 <211> 4308
 <212> DNA
 <213> Homo sapiens

<220>
 <221> unsure
 <222> 1478, 3978, 4057-4058, 4070
 <223> unknown base

<400> 527
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 tcccctcc 4308

<210> 528
 <211> 1285
 <212> DNA
 <213> Homo sapiens

<400> 528
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 ccagtggggg aattcggaga tataagtttc cgagccattg ccacaggaag 1150
 cgttcagtgt cgatgggttc atggacctag ataggctgat aacaaagctc 1200
 acaagagggt cctgaggatt caggagagac ttatggagcc agcaaagtct 1250
 tctgaagag attgcatttg agccaggtcc tgtag 1285

<210> 529
 <211> 1380
 <212> DNA
 <213> Homo sapiens

<400> 529
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 aagggcgcca gtatgacaaa gaagggaacc tgcgccctg gtggcagaat 200
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Gender	Male	Female		
Marital status	Married	Single		
Education	High school	College		
Occupation	Manager	Worker		
Income	\$10,000	\$20,000		
Health status	Good	Fair		
Stress level	Low	High		
Life satisfaction	High	Low		
Work-life balance	Good	Poor		
Family support	High	Low		
Community involvement	High	Low		
Volunteer work	Yes	No		
Charitable donations	High	Low		
Religious participation	High	Low		
Political engagement	High	Low		
Civic participation	High	Low		
Neighborhood safety	High	Low		
Local government involvement	High	Low		
Community development	High	Low		
Local business support	High	Low		
Local education support	High	Low		
Local healthcare support	High	Low		
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 Glu Asp Gly Ala Ser Lys Gly Ala Trp Leu Asn Arg Ser Ser Ile
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 80 85 90
 Ile Ser Thr Leu Asn Lys Arg Asp Tyr Ser Leu Gln Ile Gln Asn
 95 100 105
 Val Asp Val Thr Asp Asp Gly Pro Tyr Thr Cys Ser Val Gln Thr
 110 115 120
 Gln His Thr Pro Arg Thr Met Gln Val His Leu Thr Val Gln Val
 125 130 135
 Pro Pro Lys Ile Tyr Asp Ile Ser Asn Asp Met Thr Val Asn Glu
 140 145 150
 Gly Thr Asn Val Thr Leu Thr Cys Leu Ala Thr Gly Lys Pro Glu
 155 160 165
 Pro Ser Ile Ser Trp Arg His Ile Ser Pro Ser Ala Lys Pro Phe
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 185 190 195
 Ala Gly Glu Tyr Glu Cys Ser Ala Glu Asn Ala Val Ser Phe Pro
 200 205 210
 Asp Val Arg Lys Val Lys Val Val Val Asn Phe Ala Pro Thr Ile
 215 220 225
 Gln Glu Ile Lys Ser Gly Thr Val Thr Pro Gly Arg Ser Gly Leu

230	Ile Arg Cys Glu Gly Ala Gly Val Pro	235	Pro Pro Ala Phe Glu Trp	240
	245		250	255
	Tyr Lys Gly Glu Lys Lys Leu Phe Asn		Gly Gln Gln Gly Ile Ile	
	260		265	270
	Ile Gln Asn Phe Ser Thr Arg Ser Ile		Leu Thr Val Thr Asn Val	
	275		280	285
	Thr Gln Glu His Phe Gly Asn Tyr Thr		Cys Val Ala Ala Asn Lys	
	290		295	300
	Leu Gly Thr Thr Asn Ala Ser Leu Pro		Leu Asn Pro Pro Ser Thr	
	305		310	315
	Ala Gln Tyr Gly Ile Thr Gly Ser Ala		Asp Val Leu Phe Ser Cys	
	320		325	330
	Trp Tyr Leu Val Leu Thr Leu Ser Ser		Phe Thr Ser Ile Phe Tyr	
	335		340	345
	Leu Lys Asn Ala Ile Leu Gln			
	350			

<210> 613
 <211> 1797
 <212> DNA
 <213> Homo Sapien

<400> 613
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 aaataagaaa atttcaagg aggacgagct cttgagttag acccaacaag 150
 ctgcttttca ccaaattgca atggagcctt tcgaaatcaa tgttccaaag 200
 cccaagagga gaaatggggt gaacttctcc ctagctgtgg tggatcatcta 250
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 atctgcaggc gcggctccgg gtcttgaga tgtatttcct caatgacact 350
 ctggcggctg aggacagccc gtccttctcc ttgctgcagt cagcacaccc 400
 tggagaacac ctggctcagg gtgcatcgag gctgcaagtc ctgcaggccc 450
 aactcacctg ggtccgctc agccatgagc acttgctgca gcgggtagac 500
 aacttcactc agaaccagg gatgttcaga atcaaagggtg aacaaggcgc 550
 cccaggtctt caaggtcaca agggggccat gggcatgcct ggtgcccctg 600
 gcccgccggg accacctgct gagaaggag ccaagggggc tatgggacga 650

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ctggcacccc aggaccccaa ggagagaagg gcagcaaagg cgatgggggt 800
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gggtctccca ggaagcaaag gggacagggg catgaaagga gatgcagggg 900
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gtgccaaggg tgagcctggc agtgctggct cccctgggcg agcaggactt 1100
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<210> 614
<211> 520
<212> PRT
<213> Homo Sapien

<400> 614
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Thr Gln Gln Ala Ala Phe His Gln Ile Ala Met Glu Pro Phe Glu
20 25 30

Ile	Asn	Val	Pro	Lys	Pro	Lys	Arg	Arg	Asn	Gly	Val	Asn	Phe	Ser	35	40	45
Leu	Ala	Val	Val	Val	Ile	Tyr	Leu	Ile	Leu	Leu	Thr	Ala	Gly	Ala	50	55	60
Gly	Leu	Leu	Val	Val	Gln	Val	Leu	Asn	Leu	Gln	Ala	Arg	Leu	Arg	65	70	75
Val	Leu	Glu	Met	Tyr	Phe	Leu	Asn	Asp	Thr	Leu	Ala	Ala	Glu	Asp	80	85	90
Ser	Pro	Ser	Phe	Ser	Leu	Leu	Gln	Ser	Ala	His	Pro	Gly	Glu	His	95	100	105
Leu	Ala	Gln	Gly	Ala	Ser	Arg	Leu	Gln	Val	Leu	Gln	Ala	Gln	Leu	110	115	120
Thr	Trp	Val	Arg	Val	Ser	His	Glu	His	Leu	Leu	Gln	Arg	Val	Asp	125	130	135
Asn	Phe	Thr	Gln	Asn	Pro	Gly	Met	Phe	Arg	Ile	Lys	Gly	Glu	Gln	140	145	150
Gly	Ala	Pro	Gly	Leu	Gln	Gly	His	Lys	Gly	Ala	Met	Gly	Met	Pro	155	160	165
Gly	Ala	Pro	Gly	Pro	Pro	Gly	Pro	Pro	Ala	Glu	Lys	Gly	Ala	Lys	170	175	180
Gly	Ala	Met	Gly	Arg	Asp	Gly	Ala	Thr	Gly	Pro	Ser	Gly	Pro	Gln	185	190	195
Gly	Pro	Pro	Gly	Val	Lys	Gly	Glu	Ala	Gly	Leu	Gln	Gly	Pro	Gln	200	205	210
Gly	Ala	Pro	Gly	Lys	Gln	Gly	Ala	Thr	Gly	Thr	Pro	Gly	Pro	Gln	215	220	225
Gly	Glu	Lys	Gly	Ser	Lys	Gly	Asp	Gly	Gly	Leu	Ile	Gly	Pro	Lys	230	235	240
Gly	Glu	Thr	Gly	Thr	Lys	Gly	Glu	Lys	Gly	Asp	Leu	Gly	Leu	Pro	245	250	255
Gly	Ser	Lys	Gly	Asp	Arg	Gly	Met	Lys	Gly	Asp	Ala	Gly	Val	Met	260	265	270
Gly	Pro	Pro	Gly	Ala	Gln	Gly	Ser	Lys	Gly	Asp	Phe	Gly	Arg	Pro	275	280	285
Gly	Pro	Pro	Gly	Leu	Ala	Gly	Phe	Pro	Gly	Ala	Lys	Gly	Asp	Gln	290	295	300
Gly	Gln	Pro	Gly	Leu	Gln	Gly	Val	Pro	Gly	Pro	Pro	Gly	Ala	Val	305	310	315
Gly	His	Pro	Gly	Ala	Lys	Gly	Glu	Pro	Gly	Ser	Ala	Gly	Ser	Pro			

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 aaagacgttt tctttggacc aaagatctct ttcgtgattc cttgcaacaa 450
 tcaatgagaa tcttcatgta ttctggagaa caccattcct gatttccac 500
 aaactgcact acatcagtat aactgcattt ctagtttcta tatagtgcaa 550
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<210> 616
 <211> 98
 <212> PRT
 <213> Homo Sapien

<400> 616
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 20 25 30
 Lys Ile Leu Lys Asp His Asn Cys His Asn Leu Pro Glu Gly Val
 35 40 45
 Ala Asp Leu Thr Gln Ile Asp Val Asn Val Gln Asp His Phe Trp
 50 55 60
 Asp Gly Lys Gly Cys Glu Met Ile Cys Tyr Cys Asn Phe Ser Glu
 65 70 75
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 80 85 90
 Phe Val Ile Pro Cys Asn Asn Gln
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<210> 617
 <211> 2558
 <212> DNA
 <213> Homo Sapien

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 accccgccgt ggtggttggg gggcgcgag tagagcagca gcacaggcgc 150
 gggccccggg aggccggctc tgctcgcgcc gagatgtgga atctccttca 200
 cgaaaccgac tcggctgtgg ccaccgcgcg ccgccccgcg tggctgtgcg 250
 ctggggcgct ggtgctggcg ggtggcttct ttctcctcgg cttcctcttc 300

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 tcttacataa ttttacacag ataccacatt tagcaggaac agaacaaaac 450
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 aacacatcat tatttgaacc acctcctcca ggatatgaaa atgtttcgga 650
 tattgtacca cctttcagtg ctttctctcc tcaaggaatg ccagagggcg 700
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 ccaagtattc ctgttcatcc aattggatac tatgatgcac agaagctcct 1100
 agaaaaaatg ggtggctcag caccaccaga tagcagctgg agaggaagtc 1150
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 caatgtgata ggtactctca gaggagcagt ggaaccagac agatatgtca 1300
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 aaaggaaggg tggagaccta gaagaacaat tttgtttgca agctgggatg 1450
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acctcactgt	ggcccaggtt	cgaggaggga	tggtgtttga	1950
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gtatattgat	aaatthtaaa	attggtatat	ttgaaataaa	2550
atatataa	2558			

Gln	Leu	Ala	Lys	Gln	Ile	Gln	Ser	Gln	Trp	Lys	Glu	Phe	Gly	Leu	
				95					100					105	
Asp	Ser	Val	Glu	Leu	Ala	His	Tyr	Asp	Val	Leu	Leu	Ser	Tyr	Pro	
				110					115					120	
Asn	Lys	Thr	His	Pro	Asn	Tyr	Ile	Ser	Ile	Ile	Asn	Glu	Asp	Gly	
				125					130					135	
Asn	Glu	Ile	Phe	Asn	Thr	Ser	Leu	Phe	Glu	Pro	Pro	Pro	Pro	Gly	
				140					145					150	
Tyr	Glu	Asn	Val	Ser	Asp	Ile	Val	Pro	Pro	Phe	Ser	Ala	Phe	Ser	
				155					160					165	
Pro	Gln	Gly	Met	Pro	Glu	Gly	Asp	Leu	Val	Tyr	Val	Asn	Tyr	Ala	
				170					175					180	
Arg	Thr	Glu	Asp	Phe	Phe	Lys	Leu	Glu	Arg	Asp	Met	Lys	Ile	Asn	
				185					190					195	
Cys	Ser	Gly	Lys	Ile	Val	Ile	Ala	Arg	Tyr	Gly	Lys	Val	Phe	Arg	
				200					205					210	
Gly	Asn	Lys	Val	Lys	Asn	Ala	Gln	Leu	Ala	Gly	Ala	Lys	Gly	Val	
				215					220					225	
Ile	Leu	Tyr	Ser	Asp	Pro	Ala	Asp	Tyr	Phe	Ala	Pro	Gly	Val	Lys	
				230					235					240	
Ser	Tyr	Pro	Asp	Gly	Trp	Asn	Leu	Pro	Gly	Gly	Gly	Val	Gln	Arg	
				245					250					255	
Gly	Asn	Ile	Leu	Asn	Leu	Asn	Gly	Ala	Gly	Asp	Pro	Leu	Thr	Pro	
				260					265					270	
Gly	Tyr	Pro	Ala	Asn	Glu	Tyr	Ala	Tyr	Arg	Arg	Gly	Ile	Ala	Glu	
				275					280					285	
Ala	Val	Gly	Leu	Pro	Ser	Ile	Pro	Val	His	Pro	Ile	Gly	Tyr	Tyr	
				290					295					300	
Asp	Ala	Gln	Lys	Leu	Leu	Glu	Lys	Met	Gly	Gly	Ser	Ala	Pro	Pro	
				305					310					315	
Asp	Ser	Ser	Trp	Arg	Gly	Ser	Leu	Lys	Val	Pro	Tyr	Asn	Val	Gly	
				320					325					330	
Pro	Gly	Phe	Thr	Gly	Asn	Phe	Ser	Thr	Gln	Lys	Val	Lys	Met	His	
				335					340					345	
Ile	His	Ser	Thr	Asn	Glu	Val	Thr	Arg	Ile	Tyr	Asn	Val	Ile	Gly	
				350					355					360	
Thr	Leu	Arg	Gly	Ala	Val	Glu	Pro	Asp	Arg	Tyr	Val	Ile	Leu	Gly	
				365					370					375	
Gly	His	Arg	Asp	Ser	Trp	Val	Phe	Gly	Gly	Ile	Asp	Pro	Gln	Ser	

	380		385		390
Gly Ala Ala Val	Val His Glu Ile Val	Arg Ser Phe Gly Thr	Leu		
	395		400		405
Lys Lys Glu Gly	Trp Arg Pro Arg Arg	Thr Ile Leu Phe Ala	Ser		
	410		415		420
Trp Asp Ala Glu	Glu Phe Gly Leu Leu	Gly Ser Thr Glu Trp	Ala		
	425		430		435
Glu Glu Asn Ser	Arg Leu Leu Gln Glu	Arg Gly Val Ala Tyr	Ile		
	440		445		450
Asn Ala Asp Ser	Ser Ile Glu Gly Asn	Tyr Thr Leu Arg Val	Asp		
	455		460		465
Cys Thr Pro Leu	Met Tyr Ser Leu Val	His Asn Leu Thr Lys	Glu		
	470		475		480
Leu Lys Ser Pro	Asp Glu Gly Phe Glu	Gly Lys Ser Leu Tyr	Glu		
	485		490		495
Ser Trp Thr Lys	Lys Ser Pro Ser Pro	Glu Phe Ser Gly Met	Pro		
	500		505		510
Arg Ile Ser Lys	Leu Gly Ser Gly Asn	Asp Phe Glu Val Phe	Phe		
	515		520		525
Gln Arg Leu Gly	Ile Ala Ser Gly Arg	Ala Arg Tyr Thr Lys	Asn		
	530		535		540
Trp Glu Thr Asn	Lys Phe Ser Gly Tyr	Pro Leu Tyr His Ser	Val		
	545		550		555
Tyr Glu Thr Tyr	Glu Leu Val Glu Lys	Phe Tyr Asp Pro Met	Phe		
	560		565		570
Lys Tyr His Leu	Thr Val Ala Gln Val	Arg Gly Gly Met Val	Phe		
	575		580		585
Glu Leu Ala Asn	Ser Ile Val Leu Pro	Phe Asp Cys Arg Asp	Tyr		
	590		595		600
Ala Val Val Leu	Arg Lys Tyr Ala Asp	Lys Ile Tyr Ser Ile	Ser		
	605		610		615
Met Lys His Pro	Gln Glu Met Lys Thr	Tyr Ser Val Ser Phe	Asp		
	620		625		630
Ser Leu Phe Ser	Ala Val Lys Asn Phe	Thr Glu Ile Ala Ser	Lys		
	635		640		645
Phe Ser Glu Arg	Leu Gln Asp Phe Asp	Lys Ser Asn Pro Ile	Val		
	650		655		660
Leu Arg Met Met	Asn Asp Gln Leu Met	Phe Leu Glu Arg Ala	Phe		
	665		670		675

Ile	Asp	Pro	Leu	Gly	Leu	Pro	Asp	Arg	Pro	Phe	Tyr	Arg	His	Val
				680					685					690
Ile	Tyr	Ala	Pro	Ser	Ser	His	Asn	Lys	Tyr	Ala	Gly	Glu	Ser	Phe
				695					700					705
Pro	Gly	Ile	Tyr	Asp	Ala	Leu	Phe	Asp	Ile	Glu	Ser	Lys	Val	Asp
				710					715					720
Pro	Ser	Lys	Ala	Trp	Gly	Glu	Val	Lys	Arg	Gln	Ile	Tyr	Val	Ala
				725					730					735
Ala	Phe	Thr	Val	Gln	Ala	Ala	Ala	Glu	Thr	Leu	Ser	Glu	Val	Ala
				740					745					750

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<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

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<210> 620

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

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gaacatcagc gctcccggta attcc 25

<210> 621

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<212> DNA

<213> Artificial Sequence

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<223> Synthetic oligonucleotide probe

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<210> 622

<211> 25

<212> DNA

<213> Artificial Sequence

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<223> Synthetic oligonucleotide probe

<400> 622

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<210> 623
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<400> 624
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